GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
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ruman chemicaril m		Human secreted pro	Human immune/haema	' Human cardiovascul	Human cardiovascul	Fusarium venenatum	Human secreted pro	Human polynucleoti	Chlamydia pneumoni	Human cDNA sequenc	Human cDNA clone (Drosophila melanog	Human prostate exp	Borrelia burgdorfe	Borrelia burgdorfe	⊻east AOD9604-asso	Human immune/haema	Human immune/haema		Candida albicans p	Candida albicans e	Candida albicans p	S. cerevisiae ERG8	Arabidopsis thalia	D960			d t	G	C enco	H	B DNA	A DNA		Yeast phosphomeval	S. cerevisiae pren

ALIGNMENTS

growth regulator; enzyme; gene; ss. Meissner R, Lechelt-Kunze C; DE10057755-A1 22-NOV-2000; 2000DE-1057755 22-NOV-2000; 2000DE-1057755 23-MAY-2002. Arabidopsis thaliana. Thale cress; PMVK; phosphomevalonate kinase; plant; herbicide; (FARB) BAYER AG Location/Qualifiers 685..2202 /*tag= a /product= "PMVK"

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Matches 2396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 10-12; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding plant phosphomevalonate kinase, useful identifying modulators, potentially useful as herbicides and grovergulators -
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P-PSDB; ABB77505.
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tive 0; Mismatches
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                                                                                                                                                                                                                           GORLACH J.
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MATHEW A V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant; mapping;
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Query Match

Length

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Rameaka JG,
Garcia CA,
Hurban P;
                                                                                                                                                                                     they can be used as protein expression modulators. (I) can be used in identifying homologous or related genes, in producing compositions that modulate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physiological pathways. (I) can also be used: (I) for the genetic manipulation of cells, particularly plant cells; (2) in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress; (3) for enhancing or inhibiting production of a biosynthetic modification and for screening purposes, to generate additional copies of the nucleic state to state the strain copies of the nucleic state to state the strain copies of the nucleic state to state the strain stress of the nucleic state to state the strain stress of the nucleic state the strain strains of the strain strains.
                                                                                            acids, to generate ribozymes or antisense oligonucleotides, and as single-stranded DNA probes or as triple-stand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GARC/)
(KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
(HOFF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein -
                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence capable from any one of the 999 sequences given in AbL93236 to Abl94234. (I) have insecticide and fungicide activities, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 851; 44pp; English.
                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-267486/31.
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                                                                              web site
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SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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Kricker M,
                                           BP;
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A, Mathew AV,
                                       A; 107
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                                         G; 107
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                                         T; 0 other;
24;
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                                                                                         TCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGC
 TGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTGAGT
            TGAGTAAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTGAGT
                                           CCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCACCT
                                                                                                                                       TGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGCACCAAACTGACCCA
                                                                                                                                                                                                                                  AATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAAC
                                                                                                                                                                                       TCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid (I, ABL60244) that encodes a plant phosphomevalonate kinase (PMVK, ABB77505), excluding the known fully defined partial sequences ABL60245-ABL60247. Plant PMVK, (I), constructs and host cells that contain (I) are used to identify agents that bind to and/or modulate activity of PMVK, potentially useful as herbicides and growth regulators. (I) is also used for recombinant production of PMVK. The present sequence is that of a PMVK encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding identifying modulators, po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14-15; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meissner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-2000; 2000DE-1057755
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                                                                                                                                                                                                           AAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTG
                                                                                                                                                                                                                                                                                  CGTTTTTACGCTATTGTTAAGCCAATTCATGAAGCTATCAAGCCTGAAAGCTGGCCATGG
GAGCATGCGATACAGTATGCTATAGCTGCTCCTCATTTGGCA----ACCGAGAAGGACAAA 1020
                                                                         TCTCGGAAACATTTAACACTTCAGTGTGTATCTTCAAGTGAATCAAGGAACCCTTTTGTA
                                                                                                       TCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGTA
                                                                                                                                                                                TCTTGGACCGATGTCAAGCTAACATCTCCTCAGCTTTCCAGAGAAAGCATGTATAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            17.8%; ilarity 76.1%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 213 A; 151 C; 144
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                                                                                                                                                                                                                                                                                                                                                                                         Score 425.4; DB 24; Pred. No. 1.7e-115; 0; Mismatches 162;
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                                            Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant; metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid; genome mapping; physical mapping; positional cloning; forestry; agriculture; medicine; fermentation; plant development; pest resistance;
                                                                                                                                                                                       Pinus radiata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes plant polynucleotides encoding CC polypeptides involved in the production and modification of isoprenoids, CC such as terpenoid and steroid compounds. The polynucleotides are used CC in genome mapping, in physical mapping and in positional cloning of CC genes. The polynucleotides and polypeptides are useful in forestry and CC agriculture for manipulation of isoprenoid metabolism, in medicine for CC therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and CC chemical processing industries involving isoprenoids. In plant CC applications, manipulating isoprenoid pathways or isoprenoid composition CC may, for example, affect plant development, pest resistance, and the CC value of extractives (e.g. plane and myrcene). The ubiquitous and CC varied roles of isoprenoids make the polynucleotides attractive targets CC analogo and Anbieuod to Anbieuod a variety of fields. Ana69527 to CC Ana69690 and Anbieuod to Anbieuod and proteins used in the exemplification of the CC present invention.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 571 BP; 161 A; 129 C; 136 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 68; 164pp; English.
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29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                          TAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGACTC
                                                                                                                                                                                                                                  TCGAGAAGCCAAATGCAGGCTTGTGTGTGTGAGTACAAATGCACGGTTTTACGCGATTGTGA
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                                  TTCAGTCTGT----GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT
                                                                     AGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAAT
                                                                                                                                                                                                                                                                                     ACATGGCTGTAGTTGTCAGCTCCTGGTAAGGTTTTAATAACAGGAGCTTATCTAATTC
                                                                                                                                          AGCCACTGCGGACTAGCACAGATTCCAGTAGTTGGGCATGGCTATGGACAGATGTGAAAT
                                                                                                                                                                                                                 {\tt TTGAGAAGCCAAATCCAGGACTTGTGCTTACCACCAGCTCGCTTCTACGCCATTGTGA}
                                                                                                                                                                                                                                                                                                                                                         210;
TGCAAAATGTTGCTTCTTCAAGTAGCAATGGTAATCCTTTTGTGGAACAAGCAGTGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENESIS RES & DEV CORP LTD FLETCHER CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0215504
99US-0146441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-NZ00219
                                                                                                                                                                                                                                                                                                                                                                        5.6%;
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                        Score 135.2;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                           Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTD
                                                                                                                                                                                                                                                                                                                                                                            .1e-29;
                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid (I ABL60244) that encodes a plant phosphomevalonate kinase (PMVK, ABB77505), excluding the known fully defined partial sequences ABL60245-ABL60247. Plant PMVK; (I), constructs and host cells that contain (I) are used to identify agents that bind to and/or modulate activity of PMVK, potentially useful as herbicides and growth regulators. (I) is also used for recombinant production of PMVK. The present sequence is that of a PMVK encoding DNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE10057755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth
                                                                                                                                                                                                                                                                                                                             Sequence 571 BP; 161 A; 129 C; 136 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 15; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meissner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monterey pine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL60247 standard; DNA; 571
                                   482
                                                                                 422
                                                                                                                                 362
                                                                                                                                                                                 302
                                                                                                                                                                                                        743
                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                           683 AAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTTGATGACTGGAGGCTACCTTGTAC 742
                                                                                                                                                                                                                                                                     Local 210;
                                 TGCAAAATGTTGCTTCTTCAAGTAGCAATGGTAATCCTTTTGTGGAACAAGCAGTGCAAT
                                                                                                                                                                                ATGCTATAGCTGCTGC
                                                       TTCAGTCTGT----GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT
                                                                                                        TAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGACTC
                                                                                                                                AGCCACTGCGGACTAGCACAGATTCCAGTAGTTGGGCATGGCTATGGACAGATGTGAAAT
                                                                                                                                                      AGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAAT
                                                                                                                                                                                                      TCGAGAAGCCAAATGCAGGGCTTGTGTTGAGTACAAATGCACGGTTTTACGCGATTGTGA
                                                                                                                                                                                                                              ACATGGCTGTAGTTGTCTCAGCTCCTGGTAAGGTTTTAATAACAGGAGCTTATCTAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid encoding plant phosphomevalonate kinase, modulators, potentially useful as herbicides
                                                                                                                                                                                                                                                                              Conservative
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or; ds.
                                                                                                                                                                                                                                                                                                                                                    invention.
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66,5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                              103;
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                                                                                                       922
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RESULT 7
AAF22297/c
ID AAF22297;
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XX AAF22297;
XX AAF22297;
XX CONTAINAR-200
XX CONTAINAR-200
XX CONTAINAR-20
XX CONTAINAR-20
XX CONTAINAR-19
PR 13-SEP-19
PR 13-SEP-19
PR 17-SEP-19
PR 17-SEP-19
PR 17-SEP-19
PR 17-SEP-19
PR 17-SEP-19
PR 17-SEP-19
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Best Local
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells
                                                                           AAC37035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200055325-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96583 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 102; Page 716–738; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AAAACCGTATAACCGTTCGGTTCAGAGGTGCCGAACCGAACCGACCCGTAAACCGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 106; Conser
                                                                                                                                                                                                                                     CTGTCGGTTTTTTCGGTTCGGGTTTCTCGGGTTTCCTTCCGAACTCCCAGGCCTA
                                                                                                                                                                                                                                                                                                                                                                        CTCAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAA
                                                                                                                                                                                                           CCCAAATTAATTTGCCGTTCGGTTTGGTTTAATCTCTTCGGTCTAAGCCGAGAACCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                AAACCCGAAGTAATCGATCGATAACTGATTACCAAACCGACCCAAACCGACATCTGATTG
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                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokines, antibodies, and growth factors
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99US-0134770.
99US-0153584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%;
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Pred. No. 1.5e-07;
0; Mismatches 67;
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(first entry) Mailana DAM fragment SEQ ID NO: 15946. Mailana DAM fragment SEQ ID NO:	16-JUN-1999 17-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999	20-MAY-1999 21-MAY-1999 24-MAY-1999 25-MAY-1999 25-MAY-1999 27-MAY-1999 01-JUN-1999 01-JUN-1999 07-JUN-1999 07-JUN-1999 08-JUN-1999 10-JUN-1999 10-JUN-1999	30 APR-1999 04 -MAY-1999 05 -MAY-1999 06 -MAY-1999 06 -MAY-1999 07 -MAY-1999 11 -MAY-1999 14 -MAY-1999 14 -MAY-1999 14 -MAY-1999 14 -MAY-1999 18 -MAY-1999 18 -MAY-1999	25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 06-APR-1999; 16-APR-1999; 19-APR-1999; 21-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999;	is selection parties.
SEED ID NO: 15946. RE 11-UNI-1599, 19916-013997, 19916-01	990S-0139454 990S-0139454 990S-0139456 990S-0139456 990S-0139456 990S-0139457 990S-0139459 990S-0139460 990S-0139461 990S-0139463 990S-0139463 990S-0139463	99US -0.135124 99US -0.135353 99US -0.135629 99US -0.136021 99US -0.136292 99US -0.137222 99US -0.137522 99US -0.137524 99US -0.13754 99US -0.138044 99US -0.138044 99US -0.138047 99US -0.138047 99US -0.138047	99US-0132407. 99US-0132484. 99US-0132485. 99US-0132486. 99US-0132863. 99US-0134256. 99US-0134218. 99US-0134219. 99US-0134270. 99US-0134768.	99US-0121825. 99US-0123180. 99US-0125788. 99US-0125788. 99US-0126785. 99US-0126785. 99US-0128234. 99US-0128234. 99US-0128714. 99US-0130077. 99US-01300449. 99US-0130810. 99US-0131449. 99US-0131449. 99US-0131449.	ana DNA fravary; genetic ation; sign; promoter; ana.
Part District Part Dis		·			mapping; gen al transducti termination
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18-JUN-1999; 99US-0139763 21-JUN-1999; 99US-0139763 22-JUN-1999; 99US-0140053 23-JUN-1999; 99US-0140053 24-JUN-1999; 99US-0140053 28-JUN-1999; 99US-0140053 29-JUN-1999; 99US-0140053 29-JUN-1999; 99US-0142063 20-JUL-1999; 99US-0142303 00-JUL-1999; 99US-0142303 00-JUL-1999; 99US-014364 11-JUL-1999; 99US-0144005 11-JUL-1999; 99US-0145006 11-JUL-1999; 99US-0144005 11-JUL-1999; 99US-0145006 11-JUL-1999; 99US-0144005 11-JUL-1999; 99US-0144005 11-JUL-1999; 99US-0146300 11-JUL-1999; 99US-0			į.		control;
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RESULT 9
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
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    Nucleic acid
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                                                              AAL40805;
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l Similarity 98.5%;
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Pred. No. 7.7e
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   of prenyl alcohol SEQ ID
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1356

вP;

427

A; 236 C;

304 G;

389 T; 0 other;

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28-DEC-2000;
28-DEC-2000;
18-SEP-2001;
The invention relates to a method for producing prenyl alcohol comprisin culturing mutated cells, having been mutated so as to reduce the amount of transcriptional product of squalene synthase gene transcriptional activity, and then collecting prenyl alcohol from the culture medium. The method is for the production of prenyl alcohols, which is for use in industrial synthesis of isopremoid terpenoid compounds particularly physiologically-active prenyl alcohol geometric isomers. This polynuclectide sequence represents a nucleic acid sequence relating to the method for producing prenyl alcohol comprising culturing mutated
                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                      Production of prenyl alcohols by culturing translationally active mutated cells with reduced squalene synthase gene to express less
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                                                                                                                                                                                                                                                                                                                                                          transcriptional product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obata S;
                                                                                                                                                                                                                                                                                                      Page 237-238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000JP-0401701.
; 2000JP-0403067.
; 2001JP-0282978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutated cell;
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                                                                                                                                                                                                                                                                                                      262pp;
                                                                                                                                                                                                                                                                                                   Japanese.
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Query Match
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Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                          TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT
                                                                                                               GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
                                                                                                                                                                                           CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
                                                                                                                                                                                                                                    GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
TAACTTTATGGATGGGCGATATTAAGAATGGT
                                                                        ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT 790
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Pred. No. 3.7e-06;
0; Mismatches 134;
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standard;

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                        cc expression recombinant DNA for genome integration into a host contains prenyl diphosphate synthase gene or its variant; and cc (B) collecting product from the culture medium. Also described is: (1) a cm method for producing prenyl alcohol in which the expression recombinant DNA contains: (a) a hydroxymethylglutaryl-COA reductase cc gene; (2) a process for producing geranylgeraniol, comprising: (2) a process for producing geranylgeraniol comprising: (a) constructing a recombinant by transferring an expression cc recombinant DNA for genome integration into a host which cc contains hydroxymethylglutaryl-COA reductase gene or its variant; and cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc mevalonate delta-isomerase gene, mevalonate kinase gene, or cc mevalonate diphosphate decarboxylase gene. The methods are used for the production of prenyl alcohols, particularly for use in industrial cc synthesis of isoprenoid-terpenoid compounds e.g. physiologically-active represent prenyl diphosphate synthase genes and related PCR primers used in the methods of the invention
                                                                                                                                                                                                                                                                 Best Loc
Matches
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                                                                                                                                                    1397
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                                                                                                                                                                                                                                                                                                                                        Sequence 1356 BP; 427 A; 236 C; 304 G; 389 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isopentenyl diphosphate delta-isomerase; mevalonate kinase; mevalonate CoA acetyltransferase; isoprenoid-terpenoid comp
                                                                           1457
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                                       671
                                                                                                                611
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                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                        GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
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GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
                                                                                                                                                GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC 1456
                                                                                                                                                                                      ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                   CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                         CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCCATTAAATGAAGTTATTG
                                                                                                                                                                                                                                                                   138;
                                                                                                                                                                                                                                                                                                                                                                                  methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOYOTA JIDOSHA KK.
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                invention.
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ss;
                                                                                                                                                                                                                                                               ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compounds
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RESULT 11
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                                                                                                                                                             Matches
                                                                                                                                                                            Query Match
Best Local
                                                                1397
                                                                                                              1337 ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG 1396
                                                                                                                                                                                                                                                       (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is yeast phosphomevalonate kinase (PMK; ERG8) EC 2.7.4.2. encoding orf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme; transgenic plant; yeast; phosphomevalonate kinase; ERG8; PMK; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD31013 standard;
 1457 CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
                                                                                                                                                                                                                            Sequence 1356
                                                                                                                                                                                                                                                                                                                                                                                                         and isoprenoid biosynthetic pathways and inactive gene sites
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the use of specific genes of the mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 116-117; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000; 2000US-221703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001; 2001WO-US24037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast phosphomevalonate kinase (ERG8) orf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD31013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathways,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KUEH/) KUEHNLE A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAHN/) HAHN F M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731
                                GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
                                                                GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAACTTTATGGATGGGCGATATTAAGAATGGT 822
                                                                                                ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                                                                                                                                             138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAAGTAACCATTTACCTTCGGGAT 790
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         providing transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuehnle AR
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                             427 A; 236 C; 304 G; 389 T; 0 other;
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                                                                                                                                                                            50.7%;
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                                                                                                                                                             0;
                                                                                                                                                                              Score 57.6;
Pred. No. 3
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                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         having increased isoprenoid
                                                                                                                                                                              3.7e-06;
                                                                                                                                                                                             DB 24;
                                                                                                                                                             134;
                                                                                                                                                             Indels
                                                                                                                                                                                          Length 1356;
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ARESULTAND STORY OF THE STORY O
                                                                                                                                                                                         and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon D DNA encoding the entire mevalonate pathway. This operon contains secretisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate transformed to the enterminate of the products of the enterminate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                           and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid production -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1517
                                                                                                    kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-COA) synthase (HMGS) and Streptomyces sp. CL190 orf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 77; Page 141-145; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic plant; yeast; phosphomevalonate kinase; HMGRt; mevalonate kinase; mevalonate diphosphate decarboxylase; mevalonate diphosphate decarboxylase; acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1577
                                                                                 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KUEH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2000; 2000US-221703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200210398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mevalonate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Operon D DNA encoding mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD31026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD31026 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAHN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoprenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to the use of specific genes of the mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMK; HMG-CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-217122/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAACTTTATGGATGGGCGATATTAAGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUEHNLE A R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAHN
                                                                                 HMG-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thal Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dimethylallyl diphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isopentenyl
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                                                                                    reductase
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                                                                                 (HMGRt)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMG-CoA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMGS; AACT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme;
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Sequence 7681 BP;

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0 other;

The invention relates to the use of specific genes of the mevalonate and isopremoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance blosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)

Claim 77; Page 127-131;

193pp;

English

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AAD31023
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Best Local Similarity
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                                                                                                        Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                              Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1397
                                                                                              production
                                                                                                                                                                                   Hahn
                                                                                                                                                                                                                                                                                                                                                                                             transgenic plant; yeast; phosphomevalonate kinase; HMGRt; mevalonate kinase; mevalonate diphosphate decarboxylase; lacetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1577
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                                                                                                                                                           WPI; 2002-217122/27.
                                                                                                                                                                                                                                              31-JUL-2000; 2000US-221703P
                                                                                                                                                                                                                                                                                              07-FEB-2002
                                                                                                                                                                                                                                                                                                                     WO200210398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Operon A DNA encoding mevalonate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD31023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD31023 standard; DNA;
                                                                                                                                                                                                            (KUEH/)
                                                                                                                                                                                                                                                                      31-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                   MVK; PMK; HMG-CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mevalonate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2002
                                                                                                                                                                                                                      (HAHN/) HAHN F M.
                                                                                                                                                                                                                                                                                                                                                                                                                                  isoprenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAACTTTATGGATGGGCGATATTAAGAATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTGGGTTTGATGTCAGCTGTGTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAATCTTTCCTTGGAGAACCTGGAAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                                                                                                                                                          KUEHNLE A R.
                                                                                                                                                                                  Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                               Arabidopsis
                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                 dimethylallyl diphosphate; antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                               isopentenyl diphosphate;
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                                                                                                                                                                                                                                                                      2001WO-US24037
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                                                                                                                                                                                                                                                                                                                                                thaliana
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Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                               herbicide resistance; DMAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                       e kinase; HMGRt;
decarboxylase; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ance; enzyme;
; HMGS; AACT;
HMG-COA; MDD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Best Local S
Matches 138
                                              Hahn
                                                                                                                                                                                                                                                                                                     transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; AACT; mevalonate kinase; mevalonate diphosphate decarboxylase; HMG-COA; MDD acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
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               WPI;
                                                                                                                                                    31-JUL-2001;
                                                                                                                                                                                  07-FEB-2002
                                                                                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                   Operon B DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD31024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD31024 standard; DNA; 7695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. Cérevisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-COA) synthase (HMGS) and HMG-COA reductase (HMGRt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding the entire mevalonate pathway. This operon contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon A DNA conditions the products of interest. The present sequence is operon A DNA conditions the products of interest.
                                                                                                                       31-JUL-2000;
                                                                            (KUEH/)
                                                                                                                                                                                                                                                                                                                                                      isoprenoid;
                                                                                          (HAHN/)
                                              ΕM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
               2002-217122/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACTTTATGGATGGGCGATATTAAGAATGGT 4609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138;
                                                                                          HAHN F M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                          KUEHNLE A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7693 BP;
                                              Kuehnle AR
                                                                                                                                                                                                                                                                                           HMG-COA
                                                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                   dimethylallyl diphosphate; antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                   isopentenyl diphosphate; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                       2000US-221703P
                                                                                                                                                    2001WO-US24037
                                                                                                                                                                                                                                                                                                                                                                                                encoding mevalonate pathway
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                           reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2212 A; 1526 C; 1794 G; 2161 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%;
                                                                                                                                                                                                                                             thaliana
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                                                                                                                                                                                                                                                                                           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                   resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                   DMAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                   enzyme;
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of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopremoid pathway derived products in the plastids of transgenic plants and microalgae, for products in the plastids of transgenic plants and microalgae, for providing transformed cells with increased isopremoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon B DNA encoding the entire mevalonate pathway. This operon contains S. cerevisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-COA) synthase (HMGS) and HMG-COA reductase (HMGRt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
Sequence 7695 BP;
                                                                                                                                                                                                                                                                                                                                                                       and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 132-136;
                                                                                                                                                                                                                                                                                                                                                                                                                               relates to the use of specific
2214 A; 1524 C; 1793 G; 2164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  genes of the mevalonate
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Matches
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810
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TAACTTTATGGATGGGCGATATTAAGAATGGT
                                TGAATCTTTCCTTGGAGAACCTGGAAGTGGT
                                                                                           GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA
                                                                                                                                                                    CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
                                                                                                                                                                                                      GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
                                                                                                                                                                                                                                        GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC
                                                                                                                                                                                                                                                                         ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                                                  ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT
                                                                                                                                    CCGCATTAATCTCTAATTTGCCAGATATTTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                                                                                                                                                                                                                                                                                           138;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                           2.4%;
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                             . 57.6;
No. 9
                                                                                                                                                                                                                                                                                                                                                             .8e-06
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                                                                  809
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                                                                                                                                                                      1516
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Query Match

Score

DB 24;

Length 7695;

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Chimeric -
Chimeric -
Chimeric -
                                                                                          MVK;
                                                                                                                 transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; Aumevalonate kinase; mevalonate diphosphate decarboxylase; HMG-COA;
                                                                                                                                           Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
                                                                                                                                                                                    Operon E DNA
                                                                                                                                                                                                              31-MAY-2002
                                                                                                                                                                                                                                                                   AAD31027 standard;
                                                                                                       acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
                                                                                                                                                                                                                                         AAD31027;
                                                                                          HMG-COA
                                     Arabidopsis thaliana. Streptomyces sp.
                                                                Saccharomyces cerevisiae
                                                                                                                                                                                  encoding mevalonate pathway and IPP isomerase
                                                                                                                                                                                                              (first
                                                                                          reductase;
                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                   8224
                                                                                                                                                                                                                                                                   ВP
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AACT;

Rhodobacter

capsulatus

07-FEB-2002.

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Search completed: May
Job time: 597 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.4
Best Local Similarity 50.7
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon E DNA encoding the entire mevalonate pathway. This operon contains S. cerevisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-COA) synthase (HMGS); Streptomyces sp. CL190 orf encoding HMG-COA reductase (HMGRt) and R. capsulatus DNA encoding IPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                       1397 GAAGTGGGTTTGATGTCAGCTGTGTGTGTGTGATGGAAGTCAGCGTTATGTTCGCTTTCTCTC 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAHN/)
(KUEH/)
                                                                                                                                                                                                                                                                             1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 77; Page 145-149; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hahn FM, Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2000; 2000US-221703P
                                                                                                                  1577 TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT 1608
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                                                                                                                                                                                                                                                                         CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG 1516
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GenCore version 5.1.4_p5_4578

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Title: Uperfect score: Sequence:	US-09-988 2396 1 gtcgaco	5-09-988-863A-1 196 gtcgacccacgcgtccgggcttctcaa	ttotcaaaaaaaaaaaaaaa	aaa 2396	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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chelt-Kunze,C. kinases from plants	ae; Streptophyta ophyta; eudicot; Brassicales; Bra	9	2396 bp DNA nt EP1209236.	ALIGNMENTS	AC007213	S C	ATAC009992 AP000411	AC025781 AX059497	AC006136 AC006136		59543 24	T7M24		AC007396 AB062089	AX461275	AF058825 AB018113	T17H3	AC009243 AB017060	AB01/061 AC019018	02327	0642 2391	18 00952	AP002068	AC005957	AC005398	AX461344	ABU11480 AX441246	AX441244	AC079041 AX441245	AX441242 AF429385	ID		SUMMARIES
•	ı; Embryophyta; Tracheophyta; ¿Ledons; core eudicots; sssicaceae; Arabidopsis.		linear PAT 02-JUL-2002		AC007213 Arabidops	Aral	> >	Sequ	2 2	Arabidops	AX059543 Sequence AF147263 Arabidops	AF077408 Arabidops	AC012561 Arabidops	AB062089 Arabidops	Se	AF058825 Arabidops	ACO05916 Arabidops	AC009243 Genomic s AB017060 Arabidops	AC019018 Arabidops		Arak		Arak	Arab	Arak	Sequence		Sequ		Sequ	Description		

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SITFNVEEANGQNCKPEVAKTGLGSSAMTTAVVAALLHHLGLVDLSSSCKEKKFSDL
DLYHIIQOTALCIAGGKVGSGEDVSSAVYGSHRYVPRESEVLSSAQDAGKGIPLDEVI
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                                                                                                                                                                                               /organism="Hevea brasiliensis"
/cultivar="RRIM600"
/db_xref="taxon:39A1"
                                                                                                                                                                                                                                            (05-OCT-2001) Central Revenuers Co., Wilmington, Location/Qualifiers
                                                                                                                            /codon_start=1
/product="phosphomevalonate kinase"
/protein_id="AALL8926.1"
/db_xref="GI:16417948"
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                                                                                                                                                                                                              Town, C.D. and Kaul, S.
Direct Submission
Submitted (17-AUG-2000) The Institute
Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 119420)
 prediction
                                                                                                                    Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Sep 12, 2000 this sequence version replaced gi:9945156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence.
                                      clone.
                                                                                                                                                                                                                                                                                                                                    Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F5M6 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Arabidopsis thaliana
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                                                        The orientation
                                                                                                         Address all correspondence to:at@tigr.org
                                                                                                                                                                             Direct Submission
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(Chris Burge,
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(<6251. .6529,6641. .6733,6838. .7002,7098. .7191,7285. .7353,7437. .7504,7587. .7643,7723. .7913. .7991,8146. .8226,8316. .8423,8522. .8652,8734. /gene="F5M6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6251. .9220)
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complement(3585...3630)
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
complement(2799..2818)
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KLYGAHFKEIAADAPKATKITFDNSDDED"
                                                              NHDVMQI I EVLDERARDQRL I ALLEKY HKSQKNRVLVFALYKYEAERLERFLQQRGWK
AVS I HGNKAQSERTRSLSLFKEGSCPLLVATDVAARGLD I PDVEVVI NYTFPLTTEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to p68 RNA helicase (Schizosaccharomyces
pombe) GI:173419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4364.
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complement/3470
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complement/2001
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                                      VHRIGRTGRAGKKGVAHTFFTPLNKGLAGELVNVLREAGQVVPADLLKFGTHVKKKES
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complement(6)E1
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/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F5M6.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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'(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
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                                                                                                                                                                                                            complement(join(<20180. .20774,20852. .21024,21105.
21443. .21617,21696. .21875,21963. .22067,22155. .2
22386. .23390,23481. .23566,23944. .24092))</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EINRGEVANGLNCYMKQYGVTKEEASRELRKMYVYRKKVVVEEFMNSHDHVPRQVLLR CLNIARIFDVFYTEGDGYSEPKGKIEHFMTSLYLHPIPLS" complement (14658 . 14692)
                                                                                                                                                                                                                                                                                                                            /translation="MSYFDQDDKEVLAPNSDVIAATTTATTATHGIEVATEFKPVEH
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PPRPPQPNRSILPSILAPEHNLLLLEECNAMPPVTSKNG"
complement(20180. .24092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISIMFEVFKLYGHKMSCDAFDRFRGNDGRFKESLVRDFRGMLQLFEVAHLGTPCEVI
MDEALSFTRNHLESLTSGNASTASPHLLKHIQNSLYIPRYCNIEVLVAREYISYYEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(<10947. .11246,11336. .11584,11696. .11828, 11920. .12138,12229. .12613,12713. .12983,13071. .>13334))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDAKEDVRPTGRGGRGVTAKSHVIVTSNMSVRQFLDVKYTTMNL
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MKVGVLTAGMADYAAYCFIGMEDINEKEAFEWLNSNPLIIKHLTAMFRLANDVGTYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGHDEILLKFAKLNFNFCQFHYVQELKTLTKWWRDLDLASKLPYIRDRLVESHLVALG
PYFEPHYSLGRIIVAKINMIMVVVDDTYDAYATLPQVKALTECLQSIEVSDKLPDYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQDFFVASSSKKSSDDLESSLPTPHFSPSLWGDHFLSVSLNRAVEFDELEREIETTKP
LARDKLMSSESSDKEKIRLIHLLVSMGISYHFDKEIQDILKHSFTKLDDIIVGEDDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(10947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10947. .13334)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIRLARSTNGDSN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F5M6.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(18323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MEAIRIGFGLPNVHSVPLCLTTTRCLFPRQRLLHSHTPSWKPAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="contains Pfam"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:12321305"
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.12138,12229. .12613,12713. .12983,13071. .13334))
"P5M6.5"
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AATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAAGGCACGAGAAAACTG
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EFSLSDHSPMSESYPENPDALSSPQPKYQLIRVNAKGMNDSCKWVEMFEDVRAVIFCI
SLSDYDQINITPESSGTVQYQNKMIQSKELFESMVKHPCFKDTPFILILNKYDQFEEK
LNRAPLTSCDWFSDFCPVRTNNNVQSLAYQAYFYVAMKFKLLYFSITGQKLFVWQARA
                                                                                                                                                                                                                                                                                                                              EEMADLLNCLLPPQKLKPGRYWYDKESGLWGKEGEKPDRVISSNLNFTGKLSPDASNG
NTEVYLNGREITKLELRILKLANVQCPRDTHFWYDDGXYEEEGQNNIRGNIWEKAST
RFWGALFSLPPQGGDRGTVQPSSNYRYTVPVYLEHKKIGKLLLLGIEGSGTSTIFXG
KFLYGNKFSVEELQDIKLMVQSNMYRYLSILLDGRERFEEEALSHTRGLNAVEGDSGG
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CTASTKRRKKKKSECYRCGKAKWENKETCIVCDEKYCGNCVLRAMGSMPEGRKCVSC
IGQAIDESKRSKLGKHSRVLSRLLSPLEVKQIMKAEKECTANQLRPEQLIVNGYPLKP
                                                                                                                                                                                                                        EEANDEGTVTTPQSVYTLNPRLKHFSDWLLDIIATGDLDAFFPAATREYAPLVEEVWK
DPAIQATYRRKDELHFLPDVAEYFLSRAMEVSSNEYEPSERDIVYAEGVTQGNGLAFM
RDRANVDEGFKYVREVLKWDEEKEESYLNGGGEDSFYSTDMSSSPYRPEE"
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complement(24371. .24395) /rpt_family="AT_rich" 25457. .27277 /gene="F5M6.8" /note="contains multiple PPR domains: PF01535: PPR repeat" <25457. .>27277

Query Match Best Local Similarity 1100 AGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTG Conservative 31.7%; 0; Score 759; DB 8; Pred. No. 1.4e-192; Mismatches 0 Length 119420; Indels 484; Gaps 1159 4.

CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 1219 AGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCCTTGCACCGTTTG 29019 CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 28959

AAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTGGTTGCAGCTCTGTTACATT 1279

ATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGAAGGAAAGTTTGGCTGTTCTGATC 1339 ATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAAGAAGGAAAGTTTGGCTGTTCTGATC 28839

TAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCGGAA 1399

28779

GTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCCAG GTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCCAG 1459

AAGTCTTGTCATTTGCTC-----1477 28719

AAGTCTTGTCATTTGCTCAGGTTCATAACGAGAAGTTTGTTGTATATAAATTCTCCACTA 28659 AGGTTGCAGTAACAGGTCTGCCATTAA 1504

ATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTT ATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTT 1564 28539

28599

TACCACCACTGATGAATCTT-----TACCACCACTGATGAATCTTGTAAGCAAACAATCAGACCTAAATTCTTACCTAGAAAAAC 1584 28479 1584

CTGTTGTGAACTTCACCAACTTCTTATTTCTTTGACTTCTGTGAAATCTGGTGTACTAAC TTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACACCATC 1625 28359 28419

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ОУ 1432 А			DEC. 111
Db 601 C	:	338	Db 27
ОУ 1372 С		2356 AAATAAAGTTGATTTCAAATCTTCTCA 2382	Qy
Db 541 C	GAAAACTTGCGGGAAAATA 27339	7398 TGTAAGCATTTTTATACCCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATA	Db 27
Qу 1316 -	GAAAACTTGCGGGAAAATA 2355	2296 TGTAAGCATTTTTATACCCATTGTAAGGTCTTTAACTCTTG	Qy
Db 481 G	TGGGTGCTAAATTTCTTGG 27399	27458 GTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACTTGGGTGCTAAATTTCTTGG	Db 2
ОУ 1261 с	TGGGTGCTAAATTTCTTGG 2295	2236 GTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACT	Qy
Db 421 Tv	GTGTCCAATTATTAGGTGC 27459	27518 GGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGC	рь 2
0у 1201 т	GTGTCCAATTATTAGGTGC 2235	2176 GGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCA	Qy
Db 361 G	AACCACATGTATTACTTCA 27519	27578 GAAGATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCA	Db 2
Qy 1141 G	AACCACATGTATTACTTCA 2175	2116 GAAGATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACG	Qy
Db 301 T	TTTGCCCTTGTTGGTGAGA 27579	27638 TCCGGCACCAAACTGACCCAGGCATGGAGTTCGCACAATGT	Db 2
ОУ 1081 Т	TTTGGCCTTGTTGGTGAGA 2115	2056 TCCGGCACCAAACTGACCCAGGCATGGACTTCGCACAATGTTTTGGCCTTGTTGGTGAGA	Qy
Db 241 G	TGCAATCACTTTAGGGGAT 27639	27698 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATT	Db 2
Qy 1021 G	TGCAATCACTTTAGGGGAT 2055	1996 CTTGCTGGTGTTCCTGGAGCTGGAGCTGGATTTGATGCCATATTTGCAATCACTTTAGGGGAT	Qy
Db 181 G	GAGTGCTGAAGGAGTTCTA 27699	27758 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAAT	Db 2
ФУ 964 G	GAGTGCTGAAGGAGTTCTA 1995	1936 ATAGAGCCTGAATCTCAAACTCTACATTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA	Qy
Db 121 To	AGGGACCATGGAATTGCAG 27759	27818 TCCGCATTTAGAACAAATTGACTTCATCATAATTGACCTCGAGGGACCATGGAATTGCAG	Db 2
ОУ 904 Т		1935	Qy
Db 61 To	ATATACGGGTTCCACAAAT 27819	27878 AATAATACTCGTCTGGCTGTAGAATCTTAACAGCATACATGATATACGGGTTCCCACAAAT	Db 2
QУ 844 А	1934	1935	Qy
Db 1 c	TTACTTAGTGCTGTTGCAT 27879	27938 TTGATAGTTGCTTCAGATCTCAACGGACCATTTGTGCATGATTACTTAGTGCTGTTGCAT	Db 2
. Оу 784 С	1934	1935	Qy
Matches !	TAAGTGATTTTGTTCTGTT 27939	27998 AATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTCCGGTAAGTGATTTTGTTCTGTT	Db 2
Query Mate	1934	1896 AATTCTTATGCGTCAGATGGGTGAGGGGGCTAGCGTTCC	Qy
BASE COUNT ORIGIN			63
	AAGCTATGTTGAGGATCAG 1895	1836 AATCAACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAG	ογ
FEATURES source		28118 CAGTTTGGTTCATTTGACTTTTGTATCTCATGTTTAGTGGGTGTTACATGCTACTGAACC	
JOURNAL	TGTTACATGCTACTGAACC 1835	1811AGTGGG	Qy
AUTHORS	N F	178	
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V1.V1111.		28238 AGCTAAAGACCACTGGGATGTTTAACCTACGAGTCATTAAGTCTTGTAGTGTCATTAGTTAG	K.)
SOURCE	_	746	
ACCESSION VERSION KEYWORDS	TAAACGATCTGAGCAAATT 1745 TAAACGATCTGAGCAAATT 28239	1686 GCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGAGCAAATT 	ОУ Db 2
AX441245 LOCUS DEFINITION			Db 2

	1491	AGTCAGCGTTATGTTCGCTTCTCCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACA	1432	Qy
	6		60	Db
	1431	CGGAAGTGGGTTTGATGTCAGCTGTGTCTA	1372	Q 5
	1371	AAGGAAAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGT 	1316	y Qy
	540	CTGCTTTACTTC	481	DЬ
	1315	TTGCAGCTCTGTTACATTATCTTGGAGTGGTTGACC	1261	Qy
	8		4	Db
	1260	aagtagcaaaaactggcttaggttcttctgcagcaatgacaacagctg	1201	Οу
	1200 420	GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT	1141 361	Qy Db
	360	TTACTCATACAGGAATCAGATAGAAGCACTTGGTCTTCCGTTGACACCTGA>GCAI	301	DЬ
	1140	TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG	1081	Qy
	300	GAGGCATTAGATAAACTACTCTTACAAGGTCTTGATATTACGATCTTAGGTTGCAATGAC	241	Db
	1080	AATG	1021	Qy
	240	GAAAATGCTATTCAATATACTATAGCAGCTGCACATGCAACATTTGACAAGAATAAGAAA	181	Db
-	1020	TCATTTGGCAACCGAGAAGGACA	964	Qy
	180	TCTCGGAAACATTTAACACTTCAGTGTGTATCTTCAAGTGAATCAAGGAACCCTTTTGTA	121	Db
	963	TCATTTGACTCTTCAG	904	Оу
	120	TCTTGGACCGATGTCAAGCTAACATCTCCTCAGCTTTCCAGAGAAAGCATGTATAAAATTG	61	Db
	903	AGCTCTCGAGAGAAAGCATGTATAAACTG	844	Qy
	60	CGTTTTTACGCTATTGTTAAGCCAATTCATGAAGCTATCAAGCCTGAAAGCTGGGCATGG	_	рь
	843	CGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGG	784	Qy
2;	aps	ch 17.8%; Score 425.4; DB 6; Length 728; 1 Similarity 76.1%; Pred. No. 6.3e-103; 554; Conservative 0; Mismatches 162; Indels 12; Ga	Query Mat Best Loca Matches	Z w O
		/db_xref="taxon:3335" 213 a 151 c 144 g 219	SE COUNT	BAS ORI
		Location/Qualifier e 1728 /organism="Gossypi	ATURES sourc	FE!
		Lechelt- te kinase 236-A 4 2	AUTHORS TITLE JOURNAL	,
Ď.	ophyt ;	upland cotton. Gossypium hirsutum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.	SOURCE ORGANISM	134 00 10S
2002	JUL-2	AX441245. 728 bp DNA linear PAT 02- Sequence 4 from Patent EP1209236. AX441245 AX441245.1 GI:21690241	AX441245 LOCUS DEFINITION ACCESSION VERSION	AX44 LOCU DEFI ACCE VERS

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                                                                                                                                                                                                                          GGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCATATCGGAACCAGATAGAA 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGACTCTTCAGTCT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACGAAGAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAATTAACATCA 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAATGCAGGGCTTGTGTAGAGTACAAATGCACGGGTTTTTACGCGATTGTGAAGCCAATC 810
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    TTAGGTTCTTCTGCAGCAATGACAACAG
                                                               ACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAAAACTGGC 1227
                                                                                                                         AGACACGGACTCCCTTTGACATCAGAATCATTGGCCACCCTTCCGCCTTTTGCCTCCATT 523
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                                          TCTTTCAATACTGATGATGCTAATGGAAGGAATTGTAAGCCTGAAATTGCCAAAACTGGT 583
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Patent: EP 1209236-A 3 29-MAY-2002;
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/db_xref="taxon:3880"
135 c 121 g 188 t
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71.7%;
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Patent EP1209236.
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AB011480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c~MPI7
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/WetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGGCTCATCTGCAGCAATGACAACCG
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DNA Res. 5 (2), 131-145 (1998)
98341445
                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MVA3 and the 3' clone is MCM23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarzazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/)
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/translation="MASLFSSRLGSQSLSLLINIFFIFLIFLHFASQTPPPSGSIQTL NSFAGGDSDSCSGGLASIDDHASKCSYIRSQSKCGPQGYIPYLKIFFCLFGQSPVLGH LLYLSAWLFVLFYLLGDTAASYFCPSLDSLSKVLKLSPTMAGVTLLSLGARGAPDLFSSV VSFTRSNNGDFGLNSILGGAFFVSSFVVGTICYLIGSRDVAIDRNSFIRDVVFLLVAL CCLGLIIFIGKVTIWVALCYLSIYLLYVGFLSVSHFFDRKKRMSDQILRSREDLAEMG
                                                                                                                                                                                  /note="contains similarity to unknown protein
gb|AAD25785.1
gene_id:MPI7.2"
                                                                                                                                                                                                                                                /clone_lib="Mitsui P1"
complement(3187. .4899
                                                                                                   /evidence=not_experimental
/protein_id="BAB11219.1"
/db_xref="GI:10177887"
                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                        /clone="MPI7"
                                                                                                                                                                                                                                                                                                           /chromosome="5"
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CYRFSSQVIAEFVEKGLVASLARAKQEELIKAPEVIICIPMDTRQRSSFRLQAGRNAM
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SKYISGLNFPKGLDSLPYELRLLHWENYPLQSLPQDFDFGHLVKLSMPYSQLHKLGTR
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SRLPDLLNKFSQLQWLHLKYCKNLTHVPQLPPNLQYLNVHGCSSLKTVAKPLVCSIPM
KHVNSSFIFTNCNELEQAAKEEIVVYAERKCHLLASALKRCDESCVPEILFCTSFPGC
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GKAQNLQELNLEGCTALKEMHVDMENMKFLVFLNLRGCTSLKSLPEIQLISLKTLILS
GCSKFKTFQVISDKLEALYLDGTAIKELPCDIGRLQRLVMLNMKGCKKLKRLPDSLGQ
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LQRVWEGSYKALSQKEKDALLDIACFRSQDENYVASLLDSDGPSNILEDLVNKFMINI
YAGKVDMHDTLYMLSKELGREATATDRKGRHRLWHHHTIIAVLDKNKGGSNIRSIFLD
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/db_xxef="GI:10177889"
/tanala+i---":--
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11914. .13096,13164. .13645))
/note="gene_id:mPi7.4"
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VCEEKWSK PCAVVSTALAPVLLTELYCSHYSGSQRNLILY IISGSIGLIVGILAVLTT
EKSHPPKKISLVWLLGGTTKSVTWTYWIAQELVSLLISGINFGISPSVLGLTVLAWG
NSLGDLIANVTVAFHGGNDGAQIALSGCYAGPLFNTVIGLGVPLVISSLAEYPGVYII
                                                                                   KIMGFPRNLKKLYVGGTAIRELPQLPNSLEFLNAHGCKHLKSINLDFEQLPRHFIFSN
                                                                                                                                                                  SGCTEIKCFSGVPPNIEELHLQGTRIREIPIFNATHPPKVKLDRKKLWNLLENFSDVE
                                                                                                                                                                                                                  VKDLVMLKRLILSHSLQLVECDILIYAQNIELIDLQGCTGLQRFPDTSQLQNLRVVNL
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TVQGLNVHEALQLFSQSVFGINEPEQNDRKLSMKVIDYVNGNPLALSIYGRELMGKKS
TDLVPWMQKP1SGFSMSVVVSFQDDYHNDVGLR1RCVGTWKTWNNQPDR1VERFFQCW
                                                                                                                          HIDLECVINLATVISNNHVMGKLVCLNMKYCSNLRGLPDMVSLESLKVLYLSGCSELE
                                                                                                                                                                                                                                                                                                                                        HYFPRLAIDVLVDKCVLTISENTVQMNNLIQDTCQEIFNGEIETCTRMWEPSRIRYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="disease resistance protein-like"
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OKKSTAHHRKTRPKKTQPWDIKRKPTVYAPLPPLPAEWSPFTLASDDGGAATAAGDLV
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/protein_id="BAB11220.1"
/db_xref="GI:10177888"
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INAFIDTDEEMGQELSVLLERIEGSRIALAIFSPRYTESKWCLKELAKMKERTEQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVFVDACGLQETKFFSIKQNQPLTDGARVLVVVISDEVEFYDPWFPKFLKVIQGWQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MEPPAARVTPSIKADCSHSVNIICEETVLHSLVSHLSAALRREG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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CDS

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Matches Best Query Match

233;

Conservative

0;

Local

Similarity

9.5%; 95.9%;

Length 40548;

0

Gaps

0

24896

18 GGCCGACCTTCTTCTTCCTTAAGACAACACATAATGATAGAAGCAAACTGGGGAAGA 77

78

TGAAGATGGAGTGGTGAAGAACAAAACCGTATAACCGTTCGGTTCAGAGGTGCCGAACCG 137 TGAAGATGGAGTGGTGAAGAACAAAACCGAATAACCGTTCGGTTCAGAGGTGCCGAACCG 25015

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EQEPVHSLVHDAEEETHNDQTMDIEVDSVNASAQNVGSEETSPSESDRELTWSDKSVV
                                                                                                                                                                                                GPEEIHSTSNETETRTSEVGENSMHVTGEASLVMREHSTPLEESPDVVHDIAETSVNK
SVVEEIMYEEEEAQKQKDEVSPQTFNADIPIDSYASLSSGAVEYVETHSFNDEDVAQL
                                                                                                                                                                                                                                                                                                                                                     LERLANEGTSYYPFERQLSEVSESKYSSIPDTESVCTVLEDDEKKVDENNADRETKIA
KVDMVSDNDEENNHSASDHDEENSHSASDHDEEKSHSSEDSDFDEQADSKKLHHDVAE
IVLGSGETHHEQSDMMEGETSDKGKLDEVSDSDSSLSEKEEKIRDISEDEAMLISEQV
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DLPYEPNEEKPDLKGDGFQEEFSSQQPKDPMFRRHESFSVGPSMLGGPRHDRLRPFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMDVSPVSPWRPMRHEEDEDDDADRDDSLDSGSDGAESSSPDASMTDIIPMLDELHPL
LLSEAPTRGIVDGEGSDAASEGPHRSSSDEGMESDGDSESHGEEGDNENEDEEEDEEE
EDEEEKQEKKEDKDDESKSAIKWTEADQRNVMDLGSLELERNQRLENLIARRRARHNM
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RDAREAMLREREEIEKLRNMTEQERRDWERKNPKPLSAQPKKKWNFMQKYYHKGAFFQ
ADPDDEAGSAGTDGIFQRDFSAPTGEDRLDKSILPKVMQVKHFGRSGRTKWTHLVNED
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DDDVRMQKVSVLDRAFPKNDDLGVARKDDPRLRRLAKTKVENRDEVRADHRRIRQAEI
IYTEEEESRNQENRDEDDDEDALEERRRRIREKNLRRAQEEAALLPLEEEDEIGEEEE
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HFEIREFFECLHMK LEEEF PYLVEKNALNKAEKEEK IDKGGOCLMVVRG ICLSEEQ
XYTSVSGCVRRMLMKQILDTVTESGORVYRKCEVTAILILYGLPRLLTGY ILAHEMMH
YLRLNGYRNLNMVLEEGLCQVLGYMWLECQTYVFDTATIASSSSSSRTPLSTTTSKKV
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join(22096. .22104,22214. .22294,22391. .22507,22593.
22878. .22949,23030. .23148,23223. .23281,23363. .237
                                                                                                                                                                                                                                                                             VDLHEELGASSLPSFGELEINMARGVEDDYHHDEARAEESFITAHPSLDESAIHVLCG
LGDGDHEEPVYDSSPPSGSRFPSFSSVSSDYKPDLPEKNGEEIEENEEKEREVYSESI
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/protein_id="BAB11224.1"
/db_xref="GI:10177892"
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/protein_id="BaB1123:1"
/brotein_id="BaB1123:1"
/translation="MNEISDLRGMYHKPCYKELRHPNCYVCEKKIPRTAEGLKYHEHP
/translation="MNEISDLRGMYHKPCYKELRHPNCYVCEKKIPRTAEGLKYHEHP
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/note="emb|CAB16816.1|
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EDTRELQIALIESKKIKKIKQADERDQIKHADEREQRKHSKDHEEEEIESNEKEERRH
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/db_xref="GI:10177893"
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Score 227; DB ;
Pred. No. 1.1e-49;
Pred. No. 1.1e-49;
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RESULT 8
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Matches 210; Conser
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                                                                                                                          ATGCTATAGCTGCTGC 995
                                                                                                                                                        TTCAGTCTGT---GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT 979
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                                                                                                                                                                                                          TAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGACTC
                                                                                                                                                                                                                              AGCCACTGCGGACTAGCACAGATTCCAGTAGTTGGGCATGGCTATGGACAGATGTGAAAT
                                                                                                                                                                                                                                          AGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAAT 862
                                                                                                                                                                                                                                                                                                                                    AAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTGATGACTGGAGGCTACCTTGTAC 742
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                                                                                                      TTGCTGTTGCAGCTGC
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Sequence 5
AX441246
                    AX461344
Sequence 273
AX461344
AX461344.1
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Pinus radiata
Eukaryota; Viridiplantae; Streptophyta; Emt
Spermatophyta; Coniferopsida; Coniferales;
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  cress
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/db_xref="taxon:3347"
129 c 136 g 145
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from Patent EP1209236
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Pred. No. 5.7e-
0; Mismatches
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Pinus; Pinus.
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AUTHORS
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                                                  AUTHORS
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271 TAGTTTGGTTTTATTTTTCACGAGTTTTGCTCTTTTCATCGGCGACGACGACGACGTCGA 330
                    TTGCATTAATACTCATCTCCAATCTCTTCTGAAG
                                                                        AGAATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGTTTGAGGATCTAAATCGGAAA
                                                                                                                                                  TAGTTTTTTTTGGGCATTCACGTGTTTGGTTTCTCTCTGCAGCGGCGAC-TTTTTTACGGC
ATTTATTGATACTCATCTCCAATCTCTTCTGAAG
                                                                                                                                                                                          ATTGTGTG----
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/db_xref="taxon:3702"
341 c 264 g 648 t
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71.2%;
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Pred. No. 9.3e-22;
0; Mismatches 68
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Town,C.D. and Kaul,S. 1 (bases 1 to 89840)
Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adam Somerville, C.R. and Venter, J.C. AC004705 Arabidopsis Direct Submission Direct Submission Unpublished Arabidopsis thaliana. (bases 1 to 89840) thaliana 89840 bp chromosome DNA line 2 clone F26C24 linear PLN 11-MAR-2002 C24 map mi398, complete Research, Adams, M:D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8119. 8217)
/rpt_family=""-"
compression of the compression
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/rpt_family="AT_rich"
complement(2591..2623)
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/note="overlap with BAC clone T26I20 (AC005396:1. .8743)."
complement(977. .1852)
/gene="AL2914850"
                                                                                                 complement(9506. .9541)
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
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KLSMDSANLLNRGLNAYMRRLIEPCLSLASQQKRAVSNVSMLDFHAAMEVNPRVLGEE
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KSEFDKLCSKTVGRENISLHNRLVRSILKNASVAKSPPPRYPKKSLYGDPVFPPSPRK
CRSRKFRDRPSPLGPLGKPQSLTTTNDESMSKAQRLPMEVVSVEDGEEVEQMTGSPSV
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/db_xref="GI:20197261"
                                                                                                                                                  complement(9363. .9416)
/rpt_family="(TAAAAA)n"
complement/orco
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/rpt_family="AT_rich"
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complement(2701
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/codon star/
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/db_xref="taxon:3702"
/chromosome="2"
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>t_family="AT_rich"
pplement(8308. .8384)
t_family="(TA)n"
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                                  family="AT_rich"
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complement(14259. .14289)
/rpt_family="."
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complement(13155. .13207)
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complement(24067. .24123)
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VMSSNSAQPYCSSQKAESSAEVYKFTLTDADIEENQEQERKVCDEEDDCIEEEVVEED
VMSSNSAQPYCSSQKAESSAEVYKFTLTDADIEENQEQERKVCDEEDDCIEEEVVEED
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/gene="At2g14830"
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18462. .18716,18946. .19017,19
20623. .20703,20991. .21014))
/gene="At2g14835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(<17324. .17729,17844. .18030,18243. .18354,
18462. .18716,18946. .19017,19802. .19896,19995. .20112,
20623. .20703,20991. .21077,21278. .21340))
/gene="At2g14835"</pre>
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/gene="At2g14835"
/note="F26C24.16; support
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complement(15170..16350)
/gene="At2g14840"
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complement(14367. .1439
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complement(13587. .13
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25464. .25603,25684. .25728))
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/codon ******
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complement(join(<22444..23006.23094..23225,23400..23874,

25464..25603.25684..>25728))

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LINISSSSHTQEGNNLPDGYSVAGNGEYSKSAVSEIVEIDVPASAGSYMKSSSPGLAA
AAARKGVPAVDRQNSETLYYADDEDGNRKKYSRRGPLRHKFLRALLPFWSSALPTLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Expressed protein"
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DGEYDQPKCCQCQATFDEGAGHQVTRLGCLHAIHTSCLVSLIKSFPPHTAPAGYYCFA
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13033. 13073
                                                                                                                                        CCYHIVYNVFTMLPDQKESEEGERSFKKAMHVHPKLPDYDQIVAHFTALRKQQQQKQF
                                                                                                                                                                           QSVFRFRESTEDERKERKRLRRKPRSTSSSSSPIAKDVDCWRYYYKGKRSRQRKECGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QELPDEEQR"
                                                                     23985. .24047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPPRKDAAKADDGSEGRYRHQRSSKMDIRKILIFIALIACMATMGILYYRLALQAIG
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13112. .13139
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). .14755
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19017,19802. .19896,19995. .
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ORGANISM
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Best Local :
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                                                             TITLE
                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCATTAATACTCATCTCCAATCTCTTCTGAAG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTCTGTCAAAACGTTAACGATCCGACTCGAGCGTCGACAGTAAGAGAAGAAGACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTATTGATACTCATCTCCAATCTCTTCTGAAG 82360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGATAGTGTGTCGATTCGTCATTGATCCAAATCGGAGAGTTTAAGGTTCGAAAATCGGAGA 8239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGTTTGAGGATCTAAATCGGAAA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195;
                                                                                                                                                                                                                Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Direct Submission Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                AC005398 92524 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 clone T6B13 map mi398, complete
                                                                                                                                                                                                                                                                                                                                           HTG
                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                          Unpublished
                                                                                                                                           Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M., Shea, M., Ronning, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                              AC005398.3
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                                                                                Lin, X.
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                                                                                                                                                                                                 (bases 1 to 92524)
                                                                                                       (bases 1 to 92524)
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TRCAAEYLGMHETVEKONLIYKIDVFLSSSLERSWKDSIIVLGTTKPFLFLSEDLKLV
SLCIDAIATKACVDVSHVEMSYTYNKKKLAEENUGADSIKARDVPHDMVEDLCELEI
DYYKRVIMNIKYKCILGGEVIGEALKAYGYRRLSGFNKGVMEGGDLVKHKTIIETLVW
LLPAEKNSVSGGFLLKLLKAVTMYNSGEVVKEQLVRRIGQQLEEASMAELLIKSHQGS
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RSCGTYGSSRSVPTVMEDEWEAVATEEEMRALKSEIAALKLQEESGRKSMDRAGVTAI
SKIRSLIMSKKIFGKKVQLQSKGGGEKNNGGGGGGSDSSESLGSMNAAEETAKTATPS
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DSYLTEIAKDPNLPASKFIDVAESVTSIPRPAHDALYRAIDMFLKEHPGITKGEKKRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAC24177.1"
/db.xref="G1:3252807"
/translation="MKFMKIGSKLDSFKTDGNNVRYVENELASDISVDVEGSRFCLHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(26952.
29327. .29388))
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/gene="At2g14820"
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71.28;
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Pred. No. 8.6e-22;
0; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.c
On Apr 18, 2002 this sequence version replaced gi:6598467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-FEB-2002) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(2577. .2675,2804. .2913,3018. .3146, 3235. .3301.3382. .3464,3835. .3916,3881. .4057,4402. 4559. .4628,4729. .4817,4895. .5587,5682. .5985))
/gene="At2g14740"
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complement join (2291 .2675,2804 .2913,3018 .3146, 3235 .3301,3382 .3463,3835 .3916 ,3981 .4057,4402 .4485, 4559 .4628,4729 .4817,4895 .5587,5682 .>5985))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="overlap with BAC c (AC004705:73373. .89840). complement(1899. .2091) /rpt_family="AT_rich"
                                                 /translation="MDPYVAKYYWSMKFFDKHAVDKYLRIGENTLMSCMIHSVEAIIY
LFGKEYLRRPTRQDLKRLLRIGELRGFLGMTGSIDCDKDSLFATNQEVCRKDVERAFG
VLQARFAIVTNPTLI"
                                                                                                                                                                                                                                                               /note="T6Bi3.5; predicted by genscan" complement(join(<7571..7686,8006..8 /gene="At2g14730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEKLKKA I SGGDMVNLNLDWREAVPHPDDRVEYELWTNSNDECGVKCDMLMEFVKDFK
GAAQ I LEKGGFTQFRPHY I TWYCPHAFTLSRQCKSQC I NKGRYCAPDPEQDFSSGYDG
KDVVVENLRQLCVYK VANETGK PWVWWDY YTDFQ I RCPMKEKKY NKECADSV I KSLGI
                                                                                                                                                                                                                complement(join(7571. .7686,8006. .8191,9280./gene="At2g14730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLKALCSGFEETTEPAICLSTDVESNECLDNNGGCWQDKSANITACKDTFRGRVCECP
TVDGVQFKGDGYSHCEPSGPGRCTINNGGCWHEERDGHAFSACVDKDSVKCECPPGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDSAIGNFGIPQYGGSMAGTVVYPKENQKSCKEFSDFSISFKSQPGALPTFLLVDRGD
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/db_xref="GI:20197384"
                                                                                                                                                                                                                                                                                                             /gene="At2g14730"
/note="mfp17
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6732. .6761)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6613. .6657)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative vacuolar sorting receptor"
/protein_id="AAM15053.1"
/db_xref="G1:20173183"
/translation="MKQLLCYLPWLLLLTLLVSPLNDARFVVEKNSLSVTSPESIKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g14740"
/note="mfr"
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         rpt_family="AT_rich"
                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                            _family="AT_rich"
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/rpt_family="AT_rich"
complement(17985...17630)
/rpt_family="AT_rich"
complement(17680...17700)
/rpt_family="AT_rich"
complement(17826...17846)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<14856. .>15944)
/gene="At2g14710"
complement/146"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(16330.
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/gene="At2g14710"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPNLPDLVETVKFSNPSYFIEGKRLVVCSRDNTGHAWIYILGDSKLISKTRIECVVDP
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/gene="At2g14710"
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KSAWAAVWLIMLSLGLAAAGAYLVYKYRLRQYMDSEIRAIMAQYMPLDSQPEVPNHTN
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VLKALCSGFEESTEPAICLSTDMETNECLDNNGGCWQDKSANITACKDTFRGKVCVCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="AAM15050.1"
/db_xref="GI:20197380"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKQLLCYLPWLLLLSLVVSPFNEARFVVEKNSLSVTSPESIKGT
HDSAIGNFGIPQYGGSMAGTVVYPKENQKSCKEFSDFSISFKSQPGALPTFLLVDRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative vacuolar sorting receptor"
/protein_id="AAM15052.1"
/db_xref="GI:20197382"
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.12282,12422. .12498,12566. .12647,12995. .13077,
.13236,13328. .13456,13617. .13726,13904. .14002)
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RESULT 11 AC005957/c LOCUS

DEFINITION

Arabidopsis

114041 bp thaliana chromosome

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clone DNA

linear PLN 11-MAR-2002 T15J14 map mi398, complete

sequence. AC005957

ACCESSION VERSION

AC005957 AC005957.3

GI:20197491

KEYWORDS

HTG.

Arabidopsis thaliana.

ORGANISM

Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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GATTGTATCTCCCGATATCGATCTGTCTCGATCATTAGCTCAAAGAGAACAAGACGGCA
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                              TTGCATTAATACTCATCTCCAATCTCTTCTGAAG 534
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complement(21993. .22079)

/rpt_family="AT_rich"

complement(22194. .22243)

/rpt_family="AT_rich"
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21865.
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18635. .18671
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/gene="At2g14700"
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VRLRVPERTLFLSWEAIGRVVNISTIAWLVIDEAVECASKKTSYGLSYETHSNLRVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAC69372.1"
/db_xref="GI:3810590"
/translation="MAAKTPVKDMADEEGLSFFVSSPIEMSFVEGSTTIATLYFSGDI
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ement(1915'
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Pred. No. 8.6e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.or
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unsley,S.D., Lin,X.,
en,M., Ronning,C.M.,
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/rpt_family="AT_rich"
complement(3450...7066)
    complement(join(<7749. .8219,8355. .8663,8888.
                                                                                                                                                                          KVSYENTTDSAVQKAPLQSSQSTYPTTSASKGKSAAASQQNGATEKSLGEKQQNGATK
GKSGHNSSIQVSAAKGSESAGTIAKSLGEKQPTVVPKSHVKKTQLASQTALRRSPRQK
                                                                                                                                                                                                                 LKVWVKŠRTKKYGTPKKĀĀĒIVSSGPQSNGTNEAQDSLSQLLGPDNPSRLRAMGRNMN
KTKLĀCFQVKSKCMĀĒMQOKODOLQQKVELQEVIDKIKNHVNFUCLLMIKANQSKOSA
EVGĒPĪSAĀRSVJQGSOPKCILMŪMĀGTDATVVEGCIISSDPDĒIVNGSRLGPTDVXVL
IDTAIVPĒAYLMRPAINMĒIMĒKAVGQMIAMPVAMCVSLĒEKLNPĒDIĀQSFVAMPAH
                                                                                                                                                                                                                                                                                              IDGETEKBAEDI NGETEKEAEDI NGETEKËADEDI NGETENEAEDI NGETENEAELQA
AEEPEGELELSGDEDVYQPKTKRQRGPTRMKDI AKDPNARVRVEYTMMGEPIGKGSVK
LASYAGALVREHVPTTI NRWTKIGEELRTLLMKSVQAKFELDEEYQKVAVLKQMGCH
RSWKSRQVTKFREAKTNQQRMNLRPKNVSPFEWRKFVKSKTSPEFKKIGSADPTEVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(3450. .3728,3810. .4172,4473. .4769,4847. .4885,4927. .5217,5452. .5532,5790. .5993,6080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<3450. .3728,3810. .4172,4473. .4769,4847. .4885,4927. .5217,5452. .5532,5790. .5993,6080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1075. .1102)
/rpt_family="AT_rich"
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                                                                             complement(7749
                                                                                                                                        TAVWRPSDEIEYMRDSLGSSIAWPKDKLVTY"
                                                                                                                                                            TSEGLKANQKCKLMDISGKKRVVGAGRVHSIDPDQKVHHVRLGENAARVWVDVVNVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(60. .82)
                                            /gene="At2g14980"
/note="mare:".
                                                                                                                                                                                                                                                                                                                                                                       /translation="masQaKQVFFLREDDSsSWHVAMRGPSRRFREKENDDVTLDIGP
LPTTVDIDVDLEKKKRGRQPKKAAATKCNDEVEYVGTIEPTAVEQTVVPVENIEEVED
                                                                                                                                                                                                                                                                                                                                                                                                              /product="En/Spm-like transposon protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At2g14970"
/note="mis"1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis
/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g14970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="T15J14.1; related to En Spm transposon family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_famil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10045
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Fraser,C.M., Somerville,C.R. and Venter,J.C.
                                        related to En
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                                      Spm transposon family of
    .>10105))
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complement(15051..15080)
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                                                                                                                                                                                                                                       /rpt_family="AT_rich"
complement(19873. .19
/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(A)n"
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/rpt_family="(A)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(15282..15304)
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complement(15639..15677)
                                        complement(2668]
                                                                               complement (25946.
                                                                                             complement(25525. .25554)
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                                                                                                                                                        complement(20898.
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18964. .18
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16934
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complement/15000
complement(26681. .27683)
/gene="At2g15000"
/note="T15J14.4; supported by full length cONA:
                                                                                                                                                                                                             /gene="At2g14990"
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                                                                                                                                      'rpt_family="(CAT)n"
                                                                                                                                                                                               note="T15J14.3; pseudogene,
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                                      family="AT_rich"
ement(26601
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                                                                                                                                                                                                                                                                                                                                                                       y="AT_rich"
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.20947)

reverse transcriptase"

.9908

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sequence - a consensus. from T23015 64288 to
nt, also present in intron 8 of Arabidopsis
for sulfate transporter GB AB012047"
complement(14535...14596)
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complement(13175. .13)
                                /rpt_family="AT_rich"
14726. .14753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRVIDMEQLLEIEAEIVETLCLFESFFPPSFFDIMVHLTVHLGREALLGGPVHFRWMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIRKDLHPQTKGKRTYLPAALWSLSKSEKKLFCKRLFDFKGPDGYCSDIARGVSLEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFSRKHYYMGHRMGLPPSHRFRNKKSWFDGKAEHRRKSRILSGLEISHNLKNFQNNFG
NFKQSTRKRKQPESDLPVRHNLDVMHYERNVVASIVSTLMHCGKSKDGVNARKDLEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFRLKTKNGWSDKSFNDLLETLPEMLPEDNVLHTSLYEVKKFLKSFDMGYQKIHACVN
DCCLFRKKYKKLQNCLKCNASRWKTNMHTGEVKKGVPQKVLRYFSIVPRLKRMFRSEE
MARDLRWHPHNKSTDGKLCHPVDSVTWDQMNAKYPLFASEERNLRLGLSTNGFNPFNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(7749. .8219,8355. .8663,8888. .10105))
/gene="At2g14980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDNGEWTYDAFSKSSFTLKAMLLWTISDFPAYGNLAGCKVKGKMACLLCGKHTESMWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNTRYSCWPVLLVNYNLPPDLCMKKENIMLTLLIPGSQQPGNSIDVYLEPLIDDLCHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD03356.1"
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                                                                                                                                                                                                                                         rpt_family="Rf:ATREP4|ATREP4 An AT-rich repetitive
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/protein_id="AAD03356.1"
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rpt_family="AT_rich"
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les 177; Conserv
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                                                                                                                                     ATCTCCAATCTCTTCTGAAGA 535
                                                                                                                                                                      TCCATCATCGATCCAAATCGGAGAGTTTGAAGTTCGAAATCGGAGAATTTATTGATACTC
                                                                                                                                                                                                     TCCGGTTTCGATCCAAATCGGAGAGTTTGAGGATCTAAATCGGAAATTGCATTAATACTC 514
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T32B20 81877 bp
Arabidopsis thaliana BAC T32B20
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complement()oin(26960. .26979,27194. .27312,27485.
/gene="At2g15000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(37029. .38609)
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/note="T15J14.6; predicte
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complement(36100. .36)
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GNLQILCSAeSGCRDTyvGYCPSGFPYGSLTNSGDvvNvYCKLGCvSSLCGALTSLQk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="T15J14.6; predicted complement(<37029. .>38609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
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ftfsspsrnlgalgctosflplysyvatsoltshlnvnlrafcelsngigkdg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="expressed protein"
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/db_xref="GI:20197493"
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join(29745. .2997)
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 Mismatches

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Pred. No. 9.1e-18;
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                   DNA
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                   linear
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               PLN 26-JUL-2000
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JOURNAL
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AF262041.1
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 81877)
Washington University Genome Sequencing Center.
The A. thaliana Genome Sequencing Project
MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing
                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                   Submitted (01-MAY-2000)
University, 4444 Forest
                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Arabidopsis thaliana
                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                  Wilson, R
                                                                                                                                                                                                                                                                                                      (bases 1 to 81877)
                                                                                                           e-mail: rwilson@watson.wustl.edu
                                                                                                                                Genome Sequencing Center
Department of Genetics, Washington
St. Louis, MO 63108, USA
                                                                                                                                                                                                   by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:7682776
                                                                                                                                                                                                                     Department of Genetics, Park Avenue, St. Louis,
                                                                                                                                                        University.
                                                                                                                                                                                                                     Washington
Missouri 63108, USA
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NOTICE: This sequence may not be the entire insert of this clone It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions

all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by This sequence was finished as follows unless otherwise noted: sequence from more than one m13 subclone

NOTES:

FEATURES

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier; as in preparation). Location/Qualifiers 1. .81877

gene source EPGVRNGLGADIAGAAGVGAGGAGVGTGVHAVGAEGPGVMGAAAGGAQIPEVGLAGLL RQLLERLPGVVPVEAPVAPRVAEVQQRAAVAEEVPSYLRMMEQLQRIGTGYFSGGTSP EEADSWRSRVERNFGSSRCPAEYRVDLAVHFLEGDAHLMWRSVTARRRQADMSWTDFV join(3511. .4334,4377. ... 6605. .7632,7686. .8304) /gene="T32B20.f" /clone="T32B20" 3511. .8304 QPAVQHGAQVQQGVQQLAHIAAAPQGYTTREIGGTSNRAITGFLAHEVCVETLLVGGV PSRAGQGGRAGCFSCGSLDHKVADCTQRAETRECYHCRERGHLRPNCPKLQRMAVTVV SQYATKAALVETAAEVEEDLQRQEVGVSPAVQPKKTQQQVAPSKGSKPAQGQKRKWDH AEFNAKYFAQEALDRMEALFLELTQGERSVREYDQEFNRLLVYAGRGMEDDQAQMRRV /product="Hypothetical protein T32B20.f"
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CDS

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complement(22005. .23540)
/gene="T32820.e"
complement(join(22005. .22139,23232./gene="T32820.e"
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QVNYKTVDHLASVMCEMAEMELRHKNFKGALELMRRATAVPTVEVRRRVAADGNEPVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQTDGQSERTIQTLEDMLRMCVLDWGGHWADHLSLVDVVREAMQDTVMLDPSGERSIY
GADYVQETTERIRVLKLNMKEAQDRHRSYADKRKRELEFEVGDGVYLKMAMLRGPNRS
ISEIKLSPRYIGPFRIVERVGPVAYRLELPDVMRAFRKVFHVSMLRKCLHKDDEVLAK
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VKAEHQVPGSMLQSLPIPDWKWDFITMDFVVGLPVSRTKDAIWVIVDRLTKSAYFLAI
RKTDGATVLAKKYVSEIVKLHGVPVSIVSDRDFKFTSAFWRAFQAEMDTKVQMSTAYH
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LNLRQRRWMELVADYDLEIAYHPSKANMYADALSCKLVGAAPGQSVEALVSEIGALRL
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TLYLQYAKLEEDYGLAKRAMKVYEEATKKVPEGQKLEMYEIYISRAAEIFGVPRTREI
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SVKELQRKILNGFWLNDDNDVDLRLARLEELMNRRPALANSVLLRQNPHNVEQWHRRV
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ELLVHHANVISGLNVDAIIRGGIRKFTDEVGMLWTSLADYYIRKNLLEKARDIYEEGM
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RFIIYERALKALPGSYKLWYAYLRERLDIVRNLPVTHPQYDSLNNTFERGLVTMHKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Hypothetical protein T32B20.g"
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                                                                                     YEENVNVEKDVGENVPPFEENVNVDDMTEGVETEGVETKGVETEDVGKCSGNMH"
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Best Local
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                                                                                                                                                                                                                                                       160
                                                                                                                                                      220
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                    GTTTCGGTTTGATCAGTTCGGTTTGAACGGTGTTTGCCGTAAACCCAGGCCTAGTTAG
                                                                                                                                CTGTCGGTTTTTTCGGTTCGGGTTTCTCCGGTTTCTCCGAACTCCCAGGCCTAGTTTG
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                                                                                                                                                                                                                                                    CTCAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAA 219
                                                                                                                                                                                                                                                                                                         AAACCGAATAAACCGATCGGTTAGTGTCTGCCGAACCGTACCGAACCGTTAACCGAAATC 12454
                                                                                                                                                                                                                                                                                                                                                                                                        125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(56115.
/gene="T32B20.b"
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35199...35310,35414...35504,35744...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFIVEGKEDQYYKLNKALYGLKQAPRAWNHKLNQILMELKFVKCSKEPSLYRKGENED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKG IRDESVDQEAEKDEEDKNDHED IQEDSALDGNV I VP IQEE I PMLRRSERQTRPPT
YLKDY ILLSELEGERLRLA IDEEPWDF SEAMELKEWREACREE ISS I EKNRTWNLVNR
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IPFVSKNGDSKLLEDVYYIPDLRSNIISLGQATEAGCDVRMRKGYLTLFDREGELLIW
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GEVVDPTEGEEDEVVMED I VIDLKLLKLQETQESENGDTQQADALMMHELVY I NEKNV
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KGKALIGCKMNRTASMRRVESLEHLQKRIRSVGDQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIVEKQTCTSCLLGKQVRQSFPQSTSYRASNPLELVHGDLCGPITPPTTANKSFGVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MKMKDTEKIDDFAGRLSEVSTKSASLGTNIEMPKLVKKFLNSLP"
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                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.2; DB 8; Pred. No. 9.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .56312)
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.36010))
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CDS CDS	CDS	FEATURES Source		TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS TITLE TOURNAL REFERENCE	DEFINITION ACCESSION VERSION KEYWORDS SOURCE
TRINGWYSLAKSNGKUSEWILSEHWKYMLDYWMIPKAKAKSEKAKSSKLESKUGLIGAH CHR* Complement(join(21252826,29092991,30663638, 40685540,56526138)) /note="gene_id:T803.2" /pseudo /codon_start=1 /evidence=not_experimental /product="transposon protein-like" complement(join(1017610508,1055110817,1092811178, 1122112021,1212212617,1270413313,1341214198)) /pseudo /codon_start=1	/clone=TB03" /clone=TB03" /clone=Lib=TAMU_BAC" /clone=Lib=TAMU_BAC" /clone=Lib=TAMU_BAC" /complement(join(8271073,13601604)) /note="gb AAF06086.1" /note="gb AAF06086.1" /complemental /country /codon_start=1 /evidence=not_experimental /protein_id="BAB01980.1" /db_xref="GI:9294129" /translation="MTRPPIVSGRSFVRGTNFESTSTSTSTGLQRPLVPQISNAQAAYI EANEQAANIEAAEQREQAAPVIRDIRVLHPLRRNGARMYEWDASIEHLVKVNFDHLAA TB0IXYMYGIAGGREGAAFVIRDIRVLHPLRRNGARMYEWDASIEHLVKVNFDHLAA TB0IXYMYGIAGGREGAAFVIRDIRVLHPLRRNGARMYEWDASIEHLVKVNFDHLAA	http://genome.wustl.edu/eddy/tkNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is F8N14 and the 3' clone is F1M23. Location/Qualifiers 154386 /organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="caxon:3702"	protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.lastate.edu/cgi-bin/sp.cgil). http://gremlinl.zool.lastate.edu/cgi-bin/sp.cgil Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis,	Direct Submission Submitted (16-MAY-2000) Yasukazu Nakamura, Kazusa DNA Research Submitted, (16-MAY-2000) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) Tel:81-438-52-3935, Fax:81-438-52-3934) Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/Kaos/cgi-bin/agd_graph.cgi?c=T803 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant	CLONE:TBU3. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (sites) Nakamura, Y. Structural Annalysis of Arabidopsis thaliana Chromosome 3. III Unpublished 2 (bases Y. Nakamura, Y.	Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T803. AP002068 BA000014 AP002068.1 GI:8051676 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:TAMU BAC
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/evidence=not_experimental
/product="replication protein A
complement(25983. .26370)
/note="gblAAF18641.1
gene_id:T803.8
similar to unknown protein"
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complement()oin(21775. .22104,22193.
22735. .22934,23012. .23141,23223. .2
23626. .23722,23887. .23952))
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terpene synthase"
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complement(join(28153...28638,28734...28824,28916...29062))
/note="contains similarity to retroelement pol"//orte="contains similarity to retroelement pol"//orte="contains similarity"//orte="contains similarity"//orte="con
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/product="helicase-like protein"
complement(join(15838. .15949,16034.
16512. .16827))
SIMFEVFRLYQHKMSCDSFVRFKGEDGRLKESLVGDVRGMLQLYQAAHLGTPSDQYIM
                             /translation="mavartyfglgtlsylhqaplflktsqSlfprpslslkpmKhDf
ycvkattksstsddlesgrpsilfspsimgdyflsvsyddsefddiareiesymkpyv
RDRLISSHNSNKDKIRLIHLLISLGISYYFESEIEMILNKAFFELDMIIAEEDDLETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental 35905. .37542
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/note="gene_id:T803.4
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.19054))
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.23310,23406.
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.21109))
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ORIGIN
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AUTHORS
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                                                                                    Vysotskaia,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S., Li,J., Kremenetskaia,I., Luros,J., Ngan,I., Gonzalez,A., Altafi,H., Araujo,R., Chao,Q., Conn,L., Conway,A.B., Dunn,P., Hansen,N., Huizar,L., Kim,C., Palm,C., Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A., and Theologis,A.
                                                                                                                                                                                     Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 96183)
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Arabidopsis thaliana chromosome
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                  Theologis, A
                                                    Unpublished
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complement(51010 .51506)
/note="gb|AAF24522.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPRFSLGRIIIAKMTIIVALNDVCDSYATYPEAKSLIDSLQRWDIEAIDELPNYSRI
VLRLILETIGEIEREMKPRGRSASVQHTIDETKSLGRAYLALSKWASEGYMPTFDEYM
EVGEVTGGMDDFALYSFIAMEDCDEKPLYEWFDSKPKILQALSVLYRINNDIVTYERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEAKSFTRNHLESLVESTTIPPHFSSHIRDALYIDRYHNMEILVARKYISFYEQEEGH
DLTLLKFGKLSENYCRLHYIQELKTLTKWWKDQDIPSNLPCVRDRIVETYFPTLGLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
9442 c 8904 g 18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSKGEVVNGVNSYMNQHGVTKEEAVEELRKMARDNYKIVMEELLTITDVPRPVLVRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="contains similarity to non-LTR retroelement reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                             GI:12039261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .43434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91.4; DB 8; Pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                                                                                                                                                                                                    1 BAC
                                                                      1 BAC T5I8 sequence
                                                                                                                                                                                                                                                                                                                                                                                        T518
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                                                                                                                                                                                                                                                                                                                                                                                    sequence,
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                                                                                                                                                                                                                                                                                                                                                                                    complete
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TITLE
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TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-APR-1999)
St., Albany, CA 94710, U
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3 (bases 1 to 96183)
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4184. .6733
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12. .1544
                                                      DALLSGLEIFKLSKNGNLAHLIRFDSTGHSVSDSKMRIIWISVGAGIAIIIFFVFLGI
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RIFRIYINNQTAAGNFDIFAHAGGKNKGIYQDYLDPVSSKNDVLWIQLGPDSSVGASG
                                                                                                                                                                                                                                                                                       PF | 00069
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/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="T518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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Submitted (05-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA On Jan 5, 2001 this sequence version replaced gi:4558586. This sequence is of BAC T518 from Arabidopsis thallana chromosome 1. In order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide a overlap between overlapping submitted clones. The 3' end of this sequence overlaps by 1000 bp the 5' end of the sequence of the BAC T17H7.
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Center, Street, Albany, CA 94710, USA
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ASSLVKEFLLPTGPGKLVLSFIPEKGSFGFVNAIEIVSVDDKLFKESVTKVGGSEVEL
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                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAAISWDAVFYMLMTAALISGLLLTTLIIEEVKTLLYGSSEEDHEVAAASTSRPPIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLFDVGGVVGGILAGYFSDQLDGRAITAGGFIYLTIPALFLYRIYGHVSMTINIILMF
VAGLFVNGPYALITTAVAADLGTHKSLKGNARALATVTAIIDGTGSVGAAIGPVLTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVGFLAAWKIPGVAPFAFCLFFTKLVSYTFLYWLPFYVSQTEIGGEQLSQETSGNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Contains eukaryotic protein kinase domain
pr||nnn69_"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           experimental
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                                     800 Buchanan
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gene

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/gene="T518.5"

complement(join(16592. .17013,17112. .17393,17480. .17836. .1816,18248. .18530,18618. .18690,18769. .18948. .19345,19448. .19580,19943. .20157))

/gene="T518.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Strong similarity to
Lycopersicon esculentum and
subtilase family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(7204 .7302,7499 .7549,7870 .7962,
8157 .8232,8340 .8456,8616 .8680,8999 .9112,9212.
9472 .9563,9891 .10014,10118 .10285,10619 .10705))
                                                                                                                                                                               APRAHIAIYKALYKREGGFAADIIAAIDQAAQDGVDIINLSITPNRRPPGIATFFNPI
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ARHFAESALSRGVLNSSQDDASPFDGEGHGTHTASVAAGNHGIPVVVAGHRLGNASGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(16592. .20157)
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KFLPASFVASMLKRLVDECAEYCGTCNDDVKPEAHQVFYSGCQAILYVLCFRMRSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:4587515"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(11227. .11491,11761. .11945,12058. .12171
12359. 12446,12540. .112623,1733. .12899,12956. .13024,
13306. .13246,13427. .13516,13598. .13708,13801. .14073.
14128. .14196,14308. .14379,14468. .14551,14659. .14775))
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/gene="T518.4"
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GSFGYLDBEYFRRQQLTEKSDVYSFGVYLFEAVCARAVINFTLPKDQINLAEMALSWQ
KORNLESIIDSNLRGNYSPESLEKYGEIAEKCLADEGKNRPMMGEVLMSLEYYLQIHE
AWLRKONGENSFSSQAVEEAPESFTLPACSNODSSETEQSQTGSALHNSA"
                                                    ALLRYYNSSLLRENGSGKIVGSASVAKIVGGMRPTYGITAPKVMYFSARGPDPEDDSF
                                                                                     IPGVGLASGTRIMHKLVLATHALRNGTTVMDAIYVGECQDSSSFDQKLVQGKILVCSY
TVRFILGVSTIKQALLTAKNLTAAGLVFYIDPSATGFQMTSSPMDIPGILISSPQDSQ
                                                                                                                                                                                                                                                                                                                                                                    PSVHFSGRESSDSKHSLTATSSQIYRTLNRSASIIRVHDSLLRNVLRKENYLKLYSYH
YLINGFSAVLTRKQADRLAAREEVENVVLDFLVEKATTHTPQFLGLPRGAWLRDGGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/protein_id="AAD25747.1"
/db_xref="G1:4587516"
/translation="MDESSLVRFVFLLCLVSSSVFCLAESDQNATVSSAVYIVTLKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDADSAEEPDDDVELDSEMNTMSTTPKHSFMRETERLLKMPSRIRPSTSPPESFLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSRAFGGFERLDTFFPFDPCLLKMSSSYISPNFNFWSMVKTTYGEDGDEELCDEVIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPRFQSQFRSLESILSHKLNPLLVCLPSVVSEFLKQAKAGGLFIVSESFIFDDLHESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSSIGEVVGSVILMMVMERMLDLDLVSGCDDSNGGMFDMELEDAVESTMNEGDEFPVG
ALKQNTSGGNVVSELLDKLMVLFFHHLESCQNSDRLDEVWHQMVFEILFKSFENYILN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKMQEVHPRVHAALHKISYLIPLAPWNLVSILAQNMRKIDKKDPSIVTYVDNLLRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMDALVDLIISLRITFCVFVVSHHEAATSGKYLDPCLNMLVRNFSQPTFKHKVSQTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
/protein_id="AAD25746.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDFERGFICAEVMKFEDLKELGNEPAVKAAGKYRQEGKTYVVQDGD11FFKFNVSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comes from this gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Similar to WO8E3.3 gi|3880615 putative GTP-binding protein from C. elegans cosmid gb|Z92773. EST gb|AA59733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T518.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7204. .10705)
VDADIMKPNLVAPGNAIWGAWSPLGIGTNDFQGERFAMESGTSMSAPHVTGIAALIKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb|U80583 proteinase TMP from is a member of the PF|00082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST gb/AA597331
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                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
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AC009526/c
                                                    REFERENCE
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Best Local S
Matches 121
    AUTHORS
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                                                                                          JOURNAL
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CDS

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15306 ATCGGTTTGTTCGGTTTGTTCGGTTTAATCCGAAATCCCAGGCCTAGTTTCG 15250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCGGTTTTTTCGGTTCGGGTTTCTCGGTTTCTTCCGAACTCCCAGGCCTAGTTTGG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTATAATTTTGCCGATCGGTTTAGCCTTCTCTTCATAGTCGGTAATCGGAACCGAAAAA 15307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACT 221
                                                                                                                                                     Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S.,
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
AC009526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC009526 108061 bp
Arabidopsis thaliana chromosome
                               Federspiel, N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC009526.4
      Altafi,H., Araujo,R.,
                                                                                             Unpublished
                                                                                                                            Walker,M.,
                                                                                                                                                                                                                                                                           (bases 1 to 108061)
                                                              (bases 1 to 108061)
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SRGDELDLVVEERRVQRIAKDARWSKSESSVAVKWSUSGESSYMMPKDESFRRRYSK
QEHHRSSDTSRGIARGSKGDELELVVEERRVQRIAKDYRWSKSDESLYVPVSDDESFR
GNEKQEMVRYQRVSDTSRGIERGSKGDGLLLLVEERRIERIERIERIERIERSKLSGTRR
IGAKRNDDDDSLFAMSTPAFRESDESSDIVDKPATSRVEMEDE IEKLAKVLKGADIN
MEROPSKALRTDYTVMFLHELKUGWRFKUDVIEWLQRODYKSNKIRI
IYTTALNVLGKSRRPVEALNVEHAMLLQISSYPDMVAYRSIAVTLOQAGHIKBLFYVI
DTMRSPPKKFRFTLEKWDPRLEDDVVYVNAVINACVQRKOWGAFWVLQQLKQRGQ
KPSPVTYGLINEVMLACEKYNLVHEEFRKMOKSSIPNALAYRVLVNTLWREGKSDEDW
KPSPVTYGLINEVMLACEKYNLVHEEFRKMOKSSIPNALAYRVLVNTLWKEGKSDEN
HTVEDMESRGIVGSAALYYDLARCLCSAGRCNEGLMVNFVNPVVLKLIENLIYKADL
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30747. .33221
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IMLKAYLQGGLFEEARELFQKMSEDGNHIKNSSDFESRVLPDTYTFNTMLDTCAEQEK
WDDFGYAYREMLRHGYHFNAKRHLRMVLEASRAGKEEVMEATWEHMRRSNRIPPSPLI
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LVGTRAVLRWYTNIATTATNETYIVGWMAPDSVSVKVSFAKFTIGNGQTRVLSLVFRA
MKNVSMASFGRIGLFGDRGHVVNIPVAVIYKIAV*
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EDDGGGGNGDSVYEVKDMKIKSGELKDETFRKRYSRQEIVSDKRNERVFKRNGEIENH
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/product="T518.6"
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/db_xref="GI:4587517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="T518.6"
                                                                                                                         Yu,G., Ecker,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:7523676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%;
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                                  Palm, C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87.4; DB 8;
Pred. No. 3.5e-12;
); Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .23254,23451. .23642,23780. .23861,23950. .2
5,24452. .24542,24632. .25305,25421. .25768)
      Huizar,L.,
                                  Conway, A.B.,
                                                                                                                         Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I BAC
      Rowley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
Conn,L., Hanser
)., Buehler,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 96183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
      Hansen,N.F.,
er,E., Dunn,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 07-APR-2000
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                                                                                                                                                                                                                   Dunn, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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1. N S. S.

gene CDS	gene CDS	gene CDS	COMMENT FEATURES	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	TITLE
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protein motif."
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Best Local Similarity
Matches 134; Conserva
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                                                                                         92391 CCTAGCTTTATCCATTAAAACATGTGTTGGTCTT 92358
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                                                                                                                               CCTAGTTTGGTTTTATTTTTCACGAGTTTTTGCTT 302
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VVRYHMSQFYYDADFADVMTETNINNRDFDYDLDDKEATE I TDGEH I TQ I GDNVANML
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ALIGNMENTS

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM ACCESSION DEFINITION TITLE JOURNAL Large scale analysis of Arabidopsis full-length cDNA (2002b) inpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh.M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Email: mseki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and Shinozaki, K. AV826684 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-06-F07 5', AV826684.1 mRNA sequence. thale cress. (bases 1 to 621) GI:19868744 EST 01-APR-2002

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RESULT 2
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AV548305
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/db_xref="taxon:3702"
/clone="RAFL09-06-F07"
/clone_lib="RAFL9"
/dev_stage="plants at various
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hr) treatments"
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/lab_host="DH10B"
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                                                                        AGTTCGGTTGAGTATACTGTTTTGCATATAGACTTGGGTGCTAAATTTCTTGGTGTAAGC 2302
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20363093
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba
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ilarity 100.0%;
Conservative
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XhoI"
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/clone="RZL51d11F"
/clone_lib="Arabidopsis thaliana
/tissue_type="roots"
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/strain="Columbia"
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GTTGATTTCAAATCTT
 AGTATACTGTTTTGCATATAGACTTGGGTGCTAAATTTCTTGGTGTAAGCATTTTTATAC 2312
                                                                                                          AGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGCACCAAACTGAC 2072
                                                                                                                                                                                                                                                                                                                            AACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                    CAGAATTCTTATGCGTCAGATGGGTGAGGCCGGCTAGCGTTCCGATAGAGCCTGAATCTCA 427
                                     CCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTG
                                                                        CCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTG 2252
                                                                                                                                                TTGCCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCA 2192
                                                                                                                                                                                  CCAGGCATGGAGTTCGCACAATGTTTTGGCCTTGTTGGTGAGAGAAGATCCACATGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.
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Kazusa DNA Research Institute
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l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone="$Q057f09F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/tissue_type="green siliques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector:
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/strain="Columbia"
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AT995676/c
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JOURNAL
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                    1874 GAGAAGCTATGTTGAGGATCAGAATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTC 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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AI995676.1 GI:5842581
EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: service@genomesystems.com
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: David Smoller, Ph.D.
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                                                                                                         Similarity
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                                                                                    Conservative
                                                                                                                                                                                      from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
weeks. Plants were grown in 1:1:1 peat
moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C
under constant light, and watered with fertilizer. cDNA
synthesis was initiated using a NotI-oligo(dT) primer.
Double-stranded cDNA was blunted, ligated to SalI adaptors
, digested with NotI, size-selected, and cloned into the
NotI and SalI sites of the pSPORT vector."

a 118 c 90 g 118 t
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/clone="701516161
                                                                                                                                                                                                                                                                                                                                                                    library was derived from untreated inflorescence tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7\,
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pSPORT; Site_1: Not1; Site_2: Sal1; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="inflorescence"
/dev_stage="4 - 7 weeks"
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Pred. No. 2e
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REFERENCE
AUTHORS
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                                                               Local Similarity hes 437; Conserv
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AV547260 Arabidopsis thallana roots Col
CDNA clone RZL28c11F 3', mRNA sequence.
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AV547260.1
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                        532-3, Kisarazu, Chiba 292-0812, asamizu@kazusa.or.jp, URL:http:,
                                                                                                                                              a
                                                                                                                                                                                           /clone_lib="Arabidopsis thaliana
/tissue_type="roots"
                                                                                                                                                                                                                                          /organism="Arabidopsis
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                                                                                                                                                                           /note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                           /clone="RZL28c11F"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                               Score 437; DB Pred. No. 1.7 0; Mismatches
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ches 0;
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CGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGG

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                                                                                                                                                                                                                                                                                                                                                                                                                                       BNI.GH19321 Six-day Cotton fiber Gossypium hirsutum cDNA to PHOSPHOMEVALONATE KINASE, mRNA sequence.
A1727861
A1727861.1 GI:5046713
                                                                                                                                                                                                                                                      Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                              upland cotton.
Gossypium hirsutum
                                                                                                                                                                                                               Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
                                                                                                                                                                                                                                                                                                             Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                  Blewitt, M., Matz, E.C., Davy, D.F.
                                                                                                                                                                                                                                            Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                       ESTS
               Similarity
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                                                                    213
                                                                                                                                                                                                                                                                                                                                   from developing
                                                                /clone_lib="Six-day Cotton fiber"
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/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
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/note="Vector: pBluescript II KS+"
                                                                                                                                                /db_xref="taxon:3635"
                                                                                                                                                              /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                         .728
               17.8%;
76.1%;
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               Score 425.4; DB 9
Pred. No. 1.1e-93;
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DNA 5' similar
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                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                         Seki,M., Narusaka,M., Ishida,J., Kamiya,A.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Arakawa,T., Shibata,K., Shinagawa,A., Muram
                                                                                                                                                                                       AV788403
AV788403.1 GI:19807193
                                                                                                                                                                                                                mRNA sequence.
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AV788403 RAFL6
          Contact: Motoaki
                     Large scale analysis of Unpublished (2002)
                                                                                                                                                                thale cress.
                                                                                                  (bases 1 to 424)
                                                 Shinozaki, K.
                                                                                                                                                                                                                          424 bp mRNA linear EST 28-MAR-2002 Arabidopsis thaliana cDNA clone RAFL06-79-G16 3',
Genomics
             Seki
                                   Arabidopsis
                                  full-length
                                                           Muramatsu,M.,
                                                                       Satou,M., Nakajima,M.,
Itoh,M., Ishii,Y.,
                                                           Hayashizaki,Y
                                   (2002b)
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                                                                      AV816420
AV816420 RAFL9 ,
mRNA sequence.
AV816420
AV816420.1 GI:
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An Arabidopsis full-length CNNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
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3-1-1 Koyadai, Tsukuba, Ibaral
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                    Arabidopsis
                                     thale cress
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/lab_host="DH10B"
/note="Site_1: SstI; Site_2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, hr) treatments"
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/db_xref="taxon:3702"
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s thaliana
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Pred. No. 2.7e-93;
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Eukaryota;

Streptophyta;

Embryophyta; Tracheophyta;

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AACC
                                                         CCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATAAAATAAAGTTGATTTCA 5
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibara Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 424)
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97 c 78 g 112 t
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/clone_lib="RAFL9"
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Query Match
Best Local Similarity 71.8
'-has 550; Conservative
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GCAAATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAGTGTGC 1798
                                                                                                                                                                                                              CACCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAGGCACGAG
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                                                                                                                                                                   CACCATCAATGGTAGGTGCTGTTAAAAAAATGGCAGAAGGCTGATCCTGAAAAATCCCCAAG
                                                                                                                                                                                                                                                                     TCTCTTTGCCACCATTAATGACACTTTTACTGGGAGAACCGGGAACCGGTGGATCATCAA
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                                                                                                                                                                                                                                                                                                                                                                     CACTAGAGGAAGTAATTGGGAACATTCTAAATGGAAAATGGGACCATGAGAGGACTGAAT 120
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                                                                           AAACATGGAGAAAGCTGGCCGATGCTAATTCAGAACTTGAGACACAACATCTTAA
                                                                                                  AAAACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGA 1738
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BF272204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm
of the cotton fiber
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/clone="GA__Eb0014D16f"
/clone_lib="Gossyplum arboreum 7-10 dpa fiber library"
/tlssue_type="Tibers isolated from bolls harvested 7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBK-CMV;
149 c 227 g 22
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/strain="AKA"
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71.8%;
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Pred. No. 1.9e-92;
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                                                                                                                                                                                                      Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
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RIKEN
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Oono,Y., Sakurai,T., Carninci,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                     /clone_lib="RAFL6" at various /dev_stage="plants at various germination to mature seeds" /lab_host="DH10B"
                                                                                                          /organism="Arabidopsis
/db_xref="taxon:3702"
/clone="RAFL06-80-003"
   /note="Site_1: SstI; Site_2:
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                                                                   Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
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                                                                                                                                                                                                                                                        Contact: Motoaki Seki
Plant Functional Genor
                                                                                                                                                                                                                                                                                        Large scale analysis of Unpublished (2002)
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                                                      site (http://www
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99.8%;
                                                  .gsc.riken.go.jp/e/plant/index _e.html)
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Pred. No. 7e-89;
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Hayashizaki,Y

Nakajima, M.,

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Buell, C.R., Hart, A., Baker,
Restrepo, S., Griffiths, H.,
                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
           Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                   Karamycheva, S.A.
Generation of a set of potato
  Email:
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/lab_host="DHIOB"
/note="Site_1: BamHI; S
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/clone_lib="RAFL9"
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/db_xref="taxon:3702"
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                                                                                                              A., Baker, B.,
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Pred. No. 1.1e-87;
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/clone="STMEC81"
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/lab_host="SOLR"
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/cultivar="Kennebec or Binjte
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Pred. No. 7.6e-82;
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MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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24833 CD4-16 Arabidopsis thaliana cDNA clone H9F5T7, mRNA sequence
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                                                                                                                                             /tissue_type="seedling hypocotyl"
/dev_stage="3 day-old"
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/dev_stage="3 day-old mRNA from 3 day-old arabidopsis thaliana (Columbia) seedling hypocotyls as template and oligo d(t) as primer, first strand synthesis was catalyzed by Moloney murine leukemia virus reverse transcriptase (Pharmacia). Second-strand cDNA was made using the procedure of Gubler and Hoffman (1983) except that DNA ligase was omitted. After the second strand reaction, the ends of the cDNA were made blunt with Klenow fragment and EcoRI/NotI adapters (Pharmacia) were ligated adapters by spun-column chromatography using sephacryl s-300 and size-fractionated on a 1% low melting point mini-gel. Size selected cDNAs (3 - 6 kb) were removed from the gel using agarase (New England Biolabs), phenol:choloroform extracted and precipitated with lug of lamidazen (Ph 7)/ethanol. A portion of each cDNA size-fraction (0.1 ug) was co-precipitated with lug of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22313tcn@ibm.cl.msu.edu
               lambdaZapII (StratageneEcoRI digested, dephosphorylated arms and then ligated in a volume of 4 ul overnight. Each ligation mix was packaged in vitro using Gigapack II gold packaging extract (Stratagene). We have determined that although first strand cDNA synthesis was initiated using dT, almost all of the cDNAs begin 8-10 bp from the poly-A
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="H9F5T7"
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Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 693.
                                                                                                           Clemson University
100 Jordan Hall, C
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1927 AGCGTTCCGATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAG-TGCTGA 1985
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                                                                             Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., D., Wood, T.C., Leslie, A. and Wilkins, T.A. An integrated analysis of the genetics, development, and evo of the cotton fiber
                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Clemson University Genomics Institute
                         Contact: Wing RA
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                                                                                                                                                                                                                                                                                                              CCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTT
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                                                                                                                                                                                                                                                                                          TCAGATAGAAGCACTTGGTCTTCCGTTGACACCCTGAGCATTGGCTACTCTACCACCGGT
                                                                  BQ118665 769 bj EST604241 mixed potato tissues 5' end, mRNA sequence.
                                           BQ118665
BQ118665.2
                     potato.
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/clone="GA_Ea0036966f"
/clone_1ib="Gossypium arboreum 7-10 dpa fiber libra
/clsue_type="Fibers isolated from bolls harvested
dpa_"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gossypium
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Pred. No. 9.3e-76;
0; Mismatches 138;
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bolls harvested 7-10
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WA clone STMEC81
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674 ACTCTTTGAAAATGGCTGTTGTTGCTTCTGCTCCTGGGAAGTTTTTGATGACTGAGGGCT 733
CACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTG
                                                                                                                                                                          ACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCAT
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                                                                                              ATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTG
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                                                  ATCGGAATCAGATTGAAGCACGTGGGCTCCCTCTTACACCTAAGTCATTGGCTTCCCTTC
                                                                                                                                              AGAGACTACTTCTGCAGGGTCTTGACATAACTATCTTGGGTTGCAATGAGTTCTATTCGT
                                                                                                                                                                                                                                               TGCAGTATGCTGTTGCAGCAGCCCATGCAACACTTGACAAAGATAAGAAGGACACATTGC
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Contact: Robin Enemic Research
The Institute for Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
On Apr 17, 2002 this sequence version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available through the Research Genetics, contact Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of a set of potato cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."

a 168 c 170 g 215 t
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/tissue_type="mixed tissues"
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/db_xref="taxon:4113"
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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!:
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       194.4
171.8
158.2
150.4
140
135.8
113.8
117.2
107.2
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1: /cgn2_6/ptodata/1/pna/P

2: /cgn2_6/ptodata/1/pna/U

3: /cgn2_6/ptodata/1/pna/U

4: /cgn2_6/ptodata/1/pna/U

5: /cgn2_6/ptodata/1/pna/U

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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/l/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/l/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/l/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/l/pna/US09_NEW_COMB.seq:*
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16 US-99-837-604A-34763
17 US-99-837-604A-3496
18 US-99-615-606A-54496
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Sequence 19, Appl
Sequence 34763, A
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Sequence 54496, A
Sequence 15, Appl
Sequence 27, Appl
Sequence 25849, A
Sequence 2518, App
Sequence 27, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 118, App
Sequence 1218, App
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1.5	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7
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US-10-240-452-67	US-09-949-016-166383	US-09-837-604A-64175	US-09-837-604A-10493	US-09-947-911-322	US-09-615-606A-49691	US-09-949-016-15821	US-10-311-455-628	PCT-US02-41115-94	US-09-837-604A-464	US-10-312-841-2	US-09-949-016-14896	US-10-311-455-882	US-09-837-604A-17362	US-09-949-016-13747	US-09-837-604A-23709	US-09-837-604A-5480	US-09-837-604A-58235	US-09-806-708B-22	US-09-675-784A-5811	US-10-391-339-5507	US-10-369-493-46489	US-10-282-122A-10932
Sequence 67, Appl	Sequence 166383,	Sequence 64175, A	Sequence 10493, A	Sequence 322, App	Sequence 49691, A	Sequence 15821, A	Sequence 628, App	Sequence 94, Appl	Sequence 464, App	Sequence 2, Appli	Sequence 14896, A	Sequence 882, App	Sequence 17362, A	Sequence 13747, A	Sequence 23709, A	Sequence 5480, Ap	Sequence 58235, A	Sequence 22, Appl	Sequence 5811, Ap	Sequence 5507, Ap	Sequence 46489, A	Sequence 10932, A

ALIGNMENTS

layo O. allene Synthesis Enzymes US CIP BER: US/09/909,745A 001-07-20 001-07-20 R: 09/433,242 -11-04 R: 60/107,241 -11-05 6 61.3%; Pred. No. 2.3e-52; ive 0; Mismatches 233; In CACACCATCAATGGTAGGTGCAGTAAAGAAA CAGAAACTAGGTAAATTGCTAAATTGCTAAATTGCTAAATTGGTGGAATTTGCAAATTGCTAAATTGGGGATTGCTAATTGAGAACTGGGAAATTGGTGGAAATTGGTGAAACTGGTAAAGAACACAATTAGCTAAAGAACACACTGGGAAGTGTTACATGCTTAAAGAACAAACTTGCTAAAGAACACACTGGGAAGAGTGGTTACATGCTTACTTCGAAAAGAGATGGTTACATGCTTAGAAACTGGGAAGGTGGGAAGGCTGCTTTCTCTAGAGGGAAGGTGGGAAGGTGGCTTCCTTAGAGGCAAGAAGAACTGTTGCTTAGAAGAACTTTGCTTAGAGGAAGCTATGTTGTTGAAAAACAAAC	Qy 1841 ACGAAGCCATTATTAA 	Qy 1781 TTAAGTCTTGTAGTGT	Qy 1721 CTAAGCTAAACGATCT	Qy 1661 ATCCAGAGAAGGCACG Db 69 ACCCTCAGAAATCCAA	Qy 1601 GAAGTGGTGGATCCTC	Query Match Best Local Similarity 61.7 Matches 369; Conservative	Sequence 21, Application US/09909745A GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Falco, S. Carl APPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: Squalene Synthesis Enz FILE REFERENCE: BB1112 US CIP CURRENT APPLICATION NUMBER: US/09/909,745A CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 09/43,242 PRIOR APPLICATION NUMBER: 09/43,242 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 26 SOFTMARE: Microsoft Office 97 SEQ ID NO 21 SEQ ID NO 21 TYPE: DNA ORGANISM: Oryza Sativa US-09-909-745A-21
mgth 757; dels 0; Gaps TGGCABATGTCTG 16 TGGLI	1841 ACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTC	TTAAGTCTTGTAGTGTGCTTACTTCTGAAAGTGGGTGTTACATGCTACTGAACCAATCA	1721 CTAAGCTAAACGATCTGAGCAAATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCA	1661 ATCCAGAGAAAGCAGAAAACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAA 1720 	1601 GAAGTGGTGGATCCTCCACACCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTG 1660 	<pre>5%; Score 229.2; DB 6; Length 757; 3%; Pred. No. 2.3e-52; 0; Mismatches 233; Indels 0;</pre>	745A thesis 9/909,7 ,242

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; ORGANISM: Lolium
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CURRENT FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 49762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 33093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33093, Application US/6 GENERAL INFORMATION:
APPLICANT: Glenn, Matthew APPLICANT: Norriss, Michael G
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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GATATTGCTACTGGGAAGTGGGATCATGAGAAGACTCGATTTTCTTTGCCTCCTCTGATG
                ACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTTACCACCACTGATG
                                                                                                                                                        AGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTCCA 1458
                                                                                                                                                                                                        CTTGACTTGGTGCATGCTATTGCTCAAAGTGCACATTGTATAGCACAAGGGAAGATTGGC 180
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                                                                  GAAATACTCTCCTCGGCTCAGGTTTCAGGAGGATGTTG---CTTGCCAGAAGTAGTAGCA
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            APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shukla, Hridayabhiranja
APPLICANT: De La Pena, Robert C.
APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid MC
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18322, Application US/10389048
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael A.
                                                                                                                                    Sequence 65010, Application US/09837604A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25129
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 18322
LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 25129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Polynucleotides, Materials Incorporating TITLE OF INVENTION: Them, and Methods for Using Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 11000.1041U1c1
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REFERENCE:
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                                                                La Rosa, Thomas J.
Shukla, Hridayabhiranjan
De La Pena, Robert C.
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(ON: Plants
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                                 Molecules And Other Molecules Associated
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                                                                                                                SEQ ID NO 19
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/433,242
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                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                             APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                                                                                                           APPLICANT: Falco, S. Carl APPLICANT: Famodu, Omola
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                                                                                                                                SOFTWARE:
                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                          PRIOR FILING DATE: 1999-11-04
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OTHER INFORMATION:
                                                                          TYPE: DNA
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TYPE: DNA
NAME/KEY: unsure LOCATION: (287)
                                                     ORGANISM: Oryza sativa
                                       FEATURE:
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Pred. No. 7.4e-33;
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; LOCATION: (533)
; OTHER INFORMATION:
US-09-909-745A-19
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OTHER INFORMATION:
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LOCATION: (460)
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                           CTTCTGGATGCCACTATGAATATGGAGGGTGTTCTACTAACTGG-ATTCCTGGGGGCCGGT
                                                    CTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGT
                                                                              ATATGCCAAGAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGAATCACAAACTCAA
                                                                                                                                 AAGAACTAATTGTTAGATCATTACTGGCCGCAAGAGATGCTTTCCNTGAAATAAGGCTTC
                                                                                                                                                          ACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTC
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US-09-837-604A-38723/c; Sequence 38723, Application US/09837604A; GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 34763
LENGTH: 388
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Sequence 34763, Application US/09837604A
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                 APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                 APPLICANT:
                                                                                                 APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shukla, Hridayabhiranjan
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CURRENT APPLICATION NUMBER: US/09/837,604A
CURRENT FILING DATE: 2001-04-18
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/197,872 PRIOR FILING DATE: 2000-04-19
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TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
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ORGANISM: Oryza sativa nipponbare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241;
                                                                                 De La Pena, Robert C.
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Shukla, Hridayabhiranjan
De La Pena, Robert C.
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62.1%;
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Pred. No. 6.3e-28;
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; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-046-Q1-K1-C9
US-09-615-606A-54496
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NUMBER OF SEQ ID NOS: 81288
SEQ ID NO 38723
LENGTH: 585
                                                                                                                                                                          SEQ ID NO 54496
 Matches 163;
                  Best Local Similarity
                                  Query Match
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/615,606A CURRENT FILING DATE: 2000-07-13 NUMBER OF SEQ ID NOS: 91669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54496, Application US/09615606P
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                                                                                                                                                                                                                                                             APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules
TITLE OF INVENTION: Plants
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PRIOR APPLICATION NUMBER: US 60/197,872
PRIOR FILING DATE: 2000-04-19
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                                                                                                                   ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                           TYPE: DNA
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                                                                                                                                                           LENGTH:
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                                                                                                                                                             296
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Shukla, Hridayabhiranjan
                                                                                                                                                                                                                                                                                                                                                    La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                        Heck,
                                                                                                                                                                                                                                                                                                                                                                                        Coombs,
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Score 113.8; DB 6
Pred. No. 9.2e-21;
0; Mismatches 82
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Pred. No. 1e-26;
0; Mismatches 1
                                  DB 6; Length
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PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 249
TYPE: DNA
ORGANISM: Zea mays
US-09-909-745A-15
                   RESULT 10
US-09-909-745A-17
Sequence 17, Application US/09909745A
GENERAL INFORMATION:
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Best Local S
Matches 160
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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PRIOR FILING DATE: 1999-11-04
APPLICANT: Falco, S. Carl
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                                                                                                                                                                                                                                                                                                       1909 CAGATGGGTGAGGCTGGCTTCCGATAGAGCCTGAATCTCAAACTCAACTTTTGGAT 1968
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                                                                                                                                                                     2029 GCCATATT 2036
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nes 160; Conserv
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                                                                                                                                                                                                                                              TCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGTGGATTTGAT 2028
                                                                                                                                                                                                                                                                                   GAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGATTCACAAACACGGCTACTAGAT 70
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Pred. No. 5.7e-19;
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; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-25849
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SEQ ID NO 25849
LENGTH: 1269
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LENGTH: 249
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hikle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xlanfeng
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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SOFTWARE: Microsoft Office 97
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ORGANISM: Zea mays
                     1209 TGAAGTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAACACAACAGCTGTGGTTGCAGC: 1268
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                                                            2.18; Local Similarity 48.48; nes 239; Conservative
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TCAAGTACATAAGACTGGTTTAGGAAGCTCGGCAGCTATGATTACAAGTCTTATAGGTTC 497
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                                                                           Score 73.6; DB 8;
Pred. No. 1.6e-09;
0; Mismatches 249
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Pred. No. 5.7e-19;
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Best Local Similarity
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APPLICANT:
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CURRENT FILING DATE: 2003-02-28
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PRIOR FILING DATE: 2002-02-21
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equence 25596, A<sub>l</sub>
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae
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1517 GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
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                                                                                                                                                                                                                           1337 ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG 1396
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                                                                                 CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG 1516
                                                                                                                       GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC 670
                                                                                                                                                             GAAGTGGGTTTGATGTCAGCTGTGTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC 1456
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                                        CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC 730
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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Pred. No. 4.2e-05;
0; Mismatches 134; Indels
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US-10-320-797-2218
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                                                                                                        Sequence 2218, Application US/10320797 GENERAL INFORMATION:
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SEQ ID NO 2218
LENGTH: 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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                 TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: 10182-021-999
                                                                    APPLICANT: Eroshkin, Alexey M. APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US02/40225
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Eroshkin, Alexey M.
APPLICANT: Zamuddio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS
TITLE OF INVENTION: METHODS OF USE
 CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 3361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Elitra Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (1313)..(1313) OTHER INFORMATION: n=g,
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OTHER INFORMATION: n=g,
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LOCATION: (1305)..(1305)
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LOCATION: (1285)..(128
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                                                       GENES OF CRYPTOCOCCUS NEOFORMANS
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SEQ ID NO 2218

LENGTH: 1506
TYPE: DNA
ORGANISM: Cryptococcus neoformans

CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: Patentin version 3.1

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; TYPE: DNA
; ORGANISM: HUMAN
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2556324)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-911-95
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DD 2311111 TTTAGGATAATGATAAACTTTTAGAATTTGTTAATACAATTTTTATAATTGAATATATCA 2311052
                                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/09947911
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
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Best Local Similarity 54.9%;
Matches 84; Conservative
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             SEQ ID NO 95
LENGTH: 25
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                     2250 TTGAGTATACTGTTTTGCATATAGACTTGGGTGCTAAATTTCTTGGTGTAAGCATTTTTA 2309
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Pred. No. 0.27;
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2370 TCAAATCTTCTCAAAAAAAAAAAAAA 2395
                                                                                                                      2310 TACCCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATAAAATAAAGTTGATT 2369
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Search completed: May Job time: 1891 secs ω, 2003, 20:27:13

Db 2310991 TAAAAGCATCCAAATCGTAACAAAAA 2310966

: NAME/KEY: misc_feature : LOCATION: (1313)..(1313) : OTHER INFORMATION: n=g, a, t or c US-10-320-797-2218

Length 1506;

NAME/KEY: misc_feature
LOCATION: (1311)..(1311)
OTHER INFORMATION: n=g, a, t or c
FEATURE:

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1305)..(1305)
OTHER INFORMATION: n=g, a

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LOCATION: (1285)..(1285)

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NAME/KEY: misc_feature .OCATION: (1285)..(128

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 192867, Sequence 4, Appli Sequence 13646, A Sequence 13678, A Sequence 5570, Ap Sequence 154090, Sequence 154090,	Sequence 83406, A Sequence 66288, A Sequence 871, App Sequence 851, App Sequence 192867,		Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1155, Ap	Description

QY 121 ICMORDSTUCCGARCCGARCCGTARACCGARACTCTCCARAGRARTICCTCARACTCACCGARCCGARCCGARCCGARCCGARCCGA	Query Match 100.0%; Score 2396; DB 37; Length 2396; Best Local Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Matches 2396; Conservative 0; Mismatches 0; Indpls 0; Ga 1 GTCGACCCACGCGTCCGGGCCGACCTTCTTCTTCTTCCTTAGACAACACATAATGATAG	RESULT 1 US-09-988-863A-1 Sequence 1, Application US/09988863A GENERAL INFORMATION: APPLICANT: Bayer AG TILE OF INVENTION: Plant phosphomevalonate kinases FILE REFERENCE: Le A 35 018 CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 SEQ ID NO 1 SEQ ID NO 4 ORGANISM: Arabidopsis thaliana FEATURE: CDS NAME/KEY: CDS LOCATION: (685)(2199) US-09-988-863A-1	c 22 400.4 16.7 840 19 US-09-532-46021 Sequence 46021, A 390 16.3 501 17 US-09-819-091A-46021 Sequence 46021, A 390 16.3 501 17 US-09-333-534-2389 Sequence 2389, Ap c 25 383.2 16.0 489 25 US-09-654-617-134754 Sequence 134754, c 26 382.8 16.0 1470 25 US-09-654-617-259014 Sequence 259014, c 27 382.8 16.0 1470 27 US-09-684-016-259014 Sequence 259014, c 28 382.8 16.0 1470 27 US-09-684-016-259014 Sequence 259014, c 28 382.8 16.0 1470 27 US-09-684-016-259014 Sequence 259014, c 29 381 15.9 417 17 US-09-333-534-14375 Sequence 181171, 31 362.4 15.1 364 27 US-09-684-016-181171 Sequence 181171, 32 358.8 15.0 421 17 US-09-333-534-16350 Sequence 181171, 31 362.4 15.1 364 27 US-09-684-016-181171 Sequence 181171, 31 362.4 15.1 369 US-09-705-926-13137 Sequence 181171, 31 362.2 12.6 1053 42 US-10-219-999-10586 Sequence 18137, A 307 12.8 105-3 42 US-10-219-999-10586 Sequence 23255, A 36 299.2 12.5 1053 42 US-10-219-999-10586 Sequence 23256, A 39 29.2 12.5 611 37 US-09-988-853A-858 Sequence 37.8 App 14.2 42.6 10.1 517 28 US-09-705-926-20673 Sequence 37.8 App 14.2 229.2 9.6 757 18 US-09-705-926-20673 Sequence 20673, A 30 205-09-688-858 Sequence 21, App1 4.5 229.2 9.6 757 18 US-09-934-859-716 Sequence 21, App1 4.5 229.2 9.5 757 34 US-09-934-859-716 Sequence 21, App1 544-520-9784 Sequence 21, App1 544-5
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RESULT 2
PCT-US02-24048A-5
; Sequence 5, Application PC/TUS0224048A
; GENERAL INFORMATION:
 APPLICANT: E.I. du Pont de Nemours &

Nemours & Company

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; TITLE OF INVENTION: brasiliensis Latex
FILE REFERENCE: CL1792 PCT
; CURRENT APPLICATION NUMBER: PCT/USO2/24048A
; CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/307,637
PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 16
; SOFTMARE: Microsoft Office 97
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                     ; TYPE: DNA
; ORGANISM: Hevea brasiliensis
US-10-036-959B-5
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                                                                                                                                                                                                                           Sequence 5, Application US/10036959B
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours & Company
APPLICANT: Hallahan, David L.
APPLICANT: Keiper-Hrynko, Natalie
TITLE OF INVENTION: Genes Involved in the Biosynthesis of Isopentenyl Diphosphate
TITLE OF INVENTION: brasiliensis Latex
FILE REFERENCE: CL-1792
                                                                         SEQ ID NO 5
LENGTH: 1509
                                                                                                                                                   CURRENT FILING DATE: 2002-05-10 PRIOR APPLICATION NUMBER: 60/307,637 PRIOR FILING DATE: 2001-07-25
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/036,959B CURRENT FILING DATE: 2002-05-10
                                                                                                                SOFTWARE: Microsoft Office 97
                                                                                                                                    NUMBER OF SEQ ID NOS:
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1761	CONCRETE TO THE TAXABLE TO THE TAXAB	1	
170:	AAGAAGTGGCAAATGTCTGATCCAGAGAAGAGCAĆGAGAAAACTGGCAGAATTTGTCAGAT 	1642 955	Qу
164: 954	CTTTTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACACCATCAATGGTAGGTGCAGTA	1582 895	Оу
158: 894	ATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGATGAAT	1522 835	D QV
152: 834	GTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTGGTACA	1462 775	Оy
146. 774	GGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCCCAGAA	1402 715	Qy Db
140: 714	GATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCGGAAGT	1342	ФУ
13 65	CTTGGAGTGGTTGACCTATCTGATCCATGTAAAGAAGGAAAGTTTGGCTGTTCTGATCTA	1282 601	Ф
128:	ACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTGGTTGCAGCTCTGTTACATTAT	1222 541	Qу ДЪ
122	TCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAA,	1162 481	Qy dd
116: 480	ATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCA	1102 421	Qy Db
110; 420	TTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCATATCGGAACCAG	1042 361	Qy Db
104: 360	ATAGCTGCTGCTCATTTGGCAACCGAGAAGGACAAAGAATCATTGCACAAACTCTTA	985 301	Ωу
984 300	CAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGTATGCT	925 241	QУ
924 240	ACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGÀCTCTT	865 181	Qy Db
180	CCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAATTA 	805 121	Qy db
804 120	GAGAAGCCAAATGCAGGGCTTGTGTTGAGTACAAATGCACGGTTTTACGCGATTGTGAAG 	745 61	ОУ
744 60	ATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTGATGACTGAGGGCTACCTTGTACTC	685	Оу
aps	atch 35.1%; Score 840.2; DB 38; Length 1509; cal Similarity 73.1%; Pred. No. 1.9e-207; 1108; Conservative 0; Mismatches 398; Indels 9; G	Query Ma Best Loc Matches	

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Matches
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SEQ ID NO 1155
LENGTH: 119420
TYPE: DNA
ORGANISM: Arabidopsis thaliana
S-09-803-736-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                            Query Match 31.7%;
Best Local Similarity 72.6%;
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                                               CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 1219
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AAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTGGTTGCAGCTCTGTTACATT
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Norris, Susan R.
                                                                                                                                                Conservative
                                                                                                                                             Score 759; DB 31;
Pred. No. 1.7e-185;
0; Mismatches 0;
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CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 121976
LENGTH: 576
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TITLE OF INVENTION:
FILE REFERENCE:
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NUMBER OF SEQ ID NOS:
SEQ ID NO 121976
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-010-10
PRIOR APPLICATION NUMBER: US 09/654
PRIOR FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kovalic, APPLICANT: Liu, Jingdong TITLE OF INVENTION:
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GAGCGTCGACAGTAAGAGAAGAAGACAGCGATTGTGTGTAGATCGACGGCGAACGTGTGT
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; LOCATION: (140)..(1675)
; OTHER INFORMATION:
US-10-219-999-9087
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US-10-219-999-9087
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PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 9087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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TITLE OF INVENTION: CDNA SEQUENCES AND USES
FILE REFERENCE: 38-10(527.6)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
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ORGANISM: Zea
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 ATAGCTGCTCATTTGGCAA---
                                                                                             ACTTCCCCTCAGCTCTCACGGGAGGCCACATACAAGCTGTCCCTAACGAAGTCGACGCTG
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Hinkle, Gregory J.
Kovalic, David K.
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Pred. No. 1.4e-123;
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-CCGAGAAGGACAAAGAATCATTGCACAAACTC 1038
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US-09-708-427-83406; Sequence 83406, Application US/09708427; GENERAL INFORMATION:
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; OTHER INFORMATION: Incyte ID No:
US-09-649-165A-2752
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LENGTH: 475
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                                              APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: THERBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Guegler, Karl
APPLICANT: Doyle, Martin
SOFTWARE: PatentIn version 3.1
           NUMBER OF SEQ ID NOS: 85364
                    CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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SOFTWARE: PERL Program
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CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/150,517
PRIOR FILING DATE: 1999-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DETECTING EXPRESSION OF FILE REFERENCE: PA-0019 US
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; OTHER INFORMATION: Ceres
US-09-708-427-83406
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Matches 922; Conserv
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                                                                                                                                                      AATACAACTAGACGAGAACTTGACTTGGTTCACTCTATTGCCCCAAAGTGCACATTGTATA
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Query Match
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                                                                                                                                                                                                                                                                                                                                              Sequence 66288, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                         SEQ ID NO 66288
                                                                                                                                                                                                     APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
 09-708-427-66288
                                                                NAME/KEY: misc_feature LOCATION: 1..1887 OTHER INFORMATION: any n
                OTHER INFORMATION: Ceres
                              NAME/KEY: misc_feature LOCATION: 1..1887
                                                                                                                                     TYPE: DNA ORGANISM: Zea mays subsp.
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PRIOR APPLICATION NUMBER: US 60/148,783
PRIOR FILING DATE: 1999-08-13
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CURRENT FILING DATE: 2000-08-11
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TITLE OF INVENTION: Expressed Sequences
TITLE OF INVENTION: thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
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Price, Jennifer L
Raines, Tracy M.
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Hurban, Patrick
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Haas, William David
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Rameaka, Joshua G.
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Slader, Ted
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sir
Matches 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(15097)D CURRENT APPLICATION NUMBER: US/09/654,617 CURRENT FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Jii
TITLE OF INVENTION:
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                         GAATCATTGCAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC 1080
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                                                                           TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG 1140
                                                                                                                                                                                                        GAGCATGCGATACAGTATGCTATAGCTGCTGCTGCTTGGCA----ACCGAGAAGGACAAA 1020
                                                                                                                                                                                                                                                                                                             TCTTGGACCGATGTCAAGCTAACATCTCCTCAGCTTTCCAGAGAAAGCATGTATAAATTG
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GCTACTCTACCACCGTTTACATCAATTACATTCAATTCTGAGGAATCAAATGGAGCAAAT
                            GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT 1200
                                                                                                                        GAGGCATTAGATAAACTACTCTTACAAGGTCTTGATATTACGATCTTAGGTTGCAATGAC
                                                                                                                                                                                      GAAAATGCTATTCAATATACTATAGCAGCTGCACATGCAACATTTGACAAGAATAAGAAA
                                                                                                                                                                                                                                                   TCTCGGAAACATTTAACACTTCAGTGTGTATCTTCAAGTGAATCAAGGAACCCTTTTGTA
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                                                            TTTTACTCATACAGGAATCAGATAGAAGCACTTGGTCTTCCGTTGACACCTGAAGCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAAGTTCACCT 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCATGGAGTTCGCACAATGTTTTGGCCTTGTTGGTGAGAGAAGATCCACATGGCGTTTG
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76.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 425.4; I Pred. No. 1.6e O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6e-99;
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; LOCATION: (1)..(728)
; OTHER INFORMATION: unsure
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HENGTH: 728
TYPE: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Jir
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                                                       GAATCATTGCACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC
                                                                                       GAAAATGCTATTCAATATACTATAGCAGCTGCACATGCAACATTTGACAAGAATAAGAAA
                                                                                                                                                                                                             TCTTGGACCGATGTCAAGCTAACATCTCCTCAGCTTTCCAGAGAAAGCATGTATAAATTG
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TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG
                                                                                                                   GAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCA----ACCGAGAAGGACAAA
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                                                                                                                                                  TCTCGGAAACATTTAACACTTCAGTGTGTATCTTCAAGTGAATCAAGGAACCCTTTTGTA
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76.1%;
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                                                                                                                                                                                                                                                                                                                                  Mismatches 162;
                                                                                                                                                                                                                                                                                                                                             Score 425.4; DB 2
Pred. No. 1.6e-99;
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Search completed: May 3, 2003, 21:11:50 Job time: 3833 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
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1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	2.1	2.4	2.4	2.4
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	Sequence 842, App	Sequence 3, Appli	Sequence 464, App	Sequence 5, Appli	Sequence 9335, Ap	Sequence 3, Appli	Sequence 202, App	Sequence 202; App	Sequence 200, App	Sequence 200, App	Sequence 201, App	Sequence 201, App	Sequence 47, Appl	Sequence 1869, Ap	Sequence 1867, Ap	Sequence 1998, Ap	Sequence 1997, Ap	Sequence 1998, Ap	Sequence 1997, Ap	Sequence 4708, Ap	Sequence 4606, Ap	Sequence 4507, Ap	Sequence 76, Appl	•	Sequence 72, Appl

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SOFTWARE: Patentin Ver.
SEO ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
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 241 GTTTCTCGGTTTCTTCCGAACTCCCAGGCCTAGTTTGGTTTTATTTTTTCACGAGTTTTGC
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                                                           GTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCGGTTTTTTTCGGTTCGG
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2340	TGCTAAATTTCTTGGTGTAAGCATTTTTATACCCATTGTAAGGTCTTTAACTCTTGGAAA	2281	Db
2340	GCTAAATTTCTTGGTGTAAGCATTTTTATACCCCATTGTAAGGTCTTTAACTCTTGGAA	2281	Qy
2280	TATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACTTGGG	2221	Db
2280	CAATTATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACT	2221	Qy
2220	ATTACTTCAGGCGTTTCATCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGT	2161	рь
2220	CATGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTTCAGTGT	2161	Оу
2160	AAAGTGGTGATCCACGAACC	2101	Db
2160	CCTTGTTGGTGAGAGAAGATCCACATGGCGTTTGCCCTAGAAAGTGGTGATCCACGAACC	2101	Qy
2100	TCACTTTAGGGGATTCCGGCACCAAACTGACCCAGGCATGGAGTTCGCACAATGTTTTG	2041	Db
2100	ATCACTTTAGGGGATTCCGGCACCAAACTGACCCAGGCATGGAGTTCGCACAATGTTTTG	2041	Qy
2040	CTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCA	1981	ф
2040	GCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGTGGATTTTGATGCCATATTTTGCA	1981	Qy
1980	AGT	1921	Db
1980	CGGCTAGCGTTCCGATAGAGCCTGAATCTCAAACTCTAACTTTTGGATTCTACAATGAGT	1921	Qy
1920	TCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTCTTATGCGTCAGATGGGTGA	1861	DЬ
1920	CTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTCTTATGCGTCAGATJGGTGAG	8	Оу
1860	ACTGAACCAATCAACGAAGCCATTATTAAAGAA	1801	Db
1860	CTTCTGAAAAGTGGGTGTTACATGCTACTGAACCAATCAACGAAGCCATTATTAAAGAA	1801	Qy
1800	TTATCTACGAGTCATTAAGTCTTGTAGTGTGCTT	1741	ממ
1800	AATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAG7GTGCTT	1741	Qy
1740	TGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGAGC	1681	Db
1740	ACTGGCAGAATTTGTCAGATGCAAATTTTAGAACTGGAAACTAAGCTAAACGATCTGAGC	1681	Qy
1680	CCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAAGGCACGAGAA	1621	Db
1680	CATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAAGGCACGAGAA	1621	Qy
1620	TCTTTACCACCACTGATCATTTCCTTTGGAGAACCTGGAAGTGGTGGATCCTCCACA	1561	Дb
1620	CTTTACCACCACTGATGAATCTTTTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACA	1561	Qy
1560	TTAAATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTC	1501	Db
1560	TAAATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTC	1501	Qy
1500	TATGTTCGCTTCTCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGGTAACAGGTCTGCCA	1441	DЬ
1500	ATGTTCGCTTCTCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCA	1441	Qy
1440	GCACAAGGGAAGGTCGGAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGT	1381	Db
1440	CACAAGGGAAGGTCGGAAGTGGGTTTGATGTCAGCTGTGTGTG	1381	Qy
1380	AAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTT	1321	Db

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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of I
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER FILING DATE: 2000-01-27
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SOFTWARE: FastSEQ for Windows Version
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LENGTH: 728
TYPE: DNA
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TITLE OF INVENTION: Plant phosphomevalonate
FILE REFERENCE: Le A 35 018
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                                                           CACCAAGAAAATAAGAATTCCACAGATCTCGATATTGTGCATATGATAGCTCAAAGTGCC
                                                                           ----AAGGAAAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAAACGTCT 1371
                                                                                                                                      GTTGCAGCTCTGTTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAG-----
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CACTGTATTGCCCAAGGTAAAGTTGGCAGTGGCTTTGATGTCAGTTCTGCTGTCTATGGG
                                                                                                                      GTTGCTGCTTTACTTCATTATCTTGGTGTTGTTAACCTTTCCACCTCTTCTGCAGATCAA
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Pred. No. 6.8e-116;
0; Mismatches 162;
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Best Local
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
ORGANISM: Medicago truncatula
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                 TTAGGTTCTTCTGCAGCAATGACAACAG 1255
                                                                                    ACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAAAACTGGC 1227
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                                                                 TCTTTCAATACTGATGATGCTAATGGAAGGAATTGTAAGCCTGAAATTGCCAAAACTGGT
                                                                                                                                    AGACACGGACTCCCTTTGACATCAGAATCATTGGCCACCCTTCCGCCTTTTGCCTCCATT 523
                                                                                                                                                                    TCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCATCAATC 1167
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Pred. No. 2.2e-
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RESULT 5 US-09-909-745-21

Sequence

21,

Application US/09909745

RESULT 6 US-09-909-745-19

Sequence 19, Application (Patent No. US20020119546A)

Application

US/09909745

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SEQ ID NO 21
LENGTH: 757
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GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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TYPE: DNA
ORGANISM: Oryza:
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
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PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
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                                                                                                AAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGT
                                                                                                                                 GGAGCTCAGCTGGTGTTCTCCCTCTTCTTGTTCGAGAAGATCCCCGAGGTGTTTCATTGG
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                                                                AAGCTGGTGACCCAAGAACAAGGGAGGTGTCAACCGCTGTATCATCGATACAAA?AAACT
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61.3%;
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Best Local 9
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LENGTH: 539
TYPE: DNA
ORGANISM: Oryza sativa
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 65/107,241
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PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
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OCATION: (287)
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                                                                                                                                                                                                             TACGATCCTGTAGTCGTCTCACGTGCAGTAAGTGGACAGAGGTGGCTACCAATCAACATC
                                                        CTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGT 2019
                                                                                        ATATGCCAAGAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGAATCACAAACTCAA
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Pred. No. 4e-34;
0; Mismatches 157;
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TYPE: DNA
ORGANISM: Pinus radiata
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APPLICATION NUMBER: US 60/258,692 FILING DATE: 2000-12-29
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Chang, H.
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Han, B.
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CURRENT APPLICATION NUMBER: US/09/988,863A
CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
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TITLE OF INVENTION: Plant phosphomevalonate kinases
FILE REFERENCE: Le A 35 018
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tent No: US20020144047a1
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; ORGANISM: Zea mays
US-09-909-745-15
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; ORGANISM: Arabidopsis thaliana
US-09-887-576-273
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Best Local Similarity
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SOFTWARE:
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
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                                                                                                                                              1849 ATTATTAAAGAACTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTCTTATGCGT 1908
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1969 TCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGTGGATTTGAT 2028
                                                         1909 CAGATGGGTGAGGCGGTTAGCGTTCCGATAGAGCCTGAATCTCAAACTTCTTGGAT 1968
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                                    GAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGATTCACAAACACGGCTACTAGAT
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for Windows Version
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                                                                                                                                                                                                                                                                            4.5%;
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Pred. No. 1.7e-21;
""Amatches 88;
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; TYPE: DNA
; ORGANISM: Zea mays
US-09-909-745-17
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Best Local Similarity
Matches 160; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09909745 Patent No. US20020119546A1
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                 APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                           APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/90 CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Falco, S. Carl APPLICANT: Famodu, Omola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/107,241
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Pred. No. 1.7e-21;
0; Mismatches 88;
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; ORGANISM: Arabidopsis thaliana
US-09-887-576-204
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4887
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SEQ ID NO 204
LENGTH: 2000
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Budworth, P.
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                                                                         1315
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                                    226
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Local Similarity 68.4%;
                 GTTTTTTCGGTTCGGGTTTCTCGGTTTCCTTCCGAACTCCCAGGCCTA 272
                                                                       TAATTTGGCCGATCGGTTCGATCTCCTTAATTCGGTTGCTGCCGAAAACCAAAATTTTCG 1374
                                                                                                          AGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCG 225
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TTTTTTCGGTTCGGGTTTCTCGGGTTGAACCGTTATCCCAGGCCTA 1421
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Chang, H.
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70.1%;
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Pred. No. 5.3e-15;
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; SEO ID NO 48
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-918-740-48
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Best Local Similarity
Matches 138; Conserv
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OTHER INFORMATION: Operon C containing A. thaliana, OTHER INFORMATION: CL190
OTHER INFORMATION: DNA, and R. capsulatus DNA-09-918-740-61
                                                                                                                                                                                   SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/09918740 Publication No. US20030033626A1
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid
TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUKKENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEC 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/918,740 CURRENT FILING DATE: 2001-07-31
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TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathway
TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/221,703 PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/918,740 CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hahn, APPLICANT: Kuehn
                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hahn,
APPLICANT: Kuehr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 76
                                                                                             LENGTH: 7681
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1337 ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG. 1396
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Best Local Similarity 50.7%;
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Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58, Application US/09918740 Publication No. US20030033626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways
TITLE OF INVENTION: Create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 58 LENGTH: 7693
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               4578 TAACTTTATGGATGGGCGATATTAAGAATGGT 4609
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                                                                                                              ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT 4577
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Pred. No. 1.1e-05;
0; Mismatches 134; Indels
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Search completed: May 3, 2003, 21:10:48 Job time : 234 secs

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                      US-08-232-463-14
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Query Match
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                CLONE: pTZgpt-
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                  REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                        TOPOLOGY: li
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441362 seqs, 153338381 residues

Scoring table:

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Database

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US-09-253-316-3
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US-09-370-601-271
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1470

Best Local Similarity Matches 23; Conserv

Conservative

213;

Pred. No. 0.0038;
13; Mismatches 177;

Indels

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5.6%;

1494 TCTGCCATTAAATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAAC 1553

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                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (1)...(65042)
; OTHER INFORMATION: n = .
US-09-784-316-3
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US-09-784-316-3
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Patent No. 6461843
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN E
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001139
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 65042
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for 
EQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/784,316
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                     44535
                                                                  44595
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                                 2284
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                                                                                                                                                    2164 TGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCA 2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1554 TGAGTTCTCTTTACCACCACTGATGAATCTTTTCCTTGGAGAACCTGGAAGTGGTGGATC 1613
                                                                                                                                                                                                                    Tocal
                               TAAATTTCTTGGTGTAAGCATTTTTATAC 2312
                                                                                                                                 TTTTTTCATTCTATTTTCTCTGTTATTCAGATTGGGTAATTTACATTGTTCTATTTTCCA 44594
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                                                                GTTCATTGATTATTTCCTCTGTCCCCTGCATTCTGTTGTTGAGCCTATCTACTGAGCTTT 44654
                                                                                                  ATTATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTTGCATATAGACTTGGGTGC 2283
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US-09-426-290-1/c

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GENERAL INFORMATION:

APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN WARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000

Sequence 1, Application US/09426290 Patent No. 6410712

SOFTWARE: 1 SEQ ID NO 1

FastSEQ for Windows Version 4.0

FEATURE:

ORGANISM: Homo Sapiens

TYPE: DNA

LENGTH: 168575

CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 24

US/09/426,290

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RESULT 4
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US-08-961-527-113
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                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                15547 GTGCCACCACTTGCAATCTTTGTCGCAACTCTTCTTTTCAAAGA 15590
                                                                                                                 15487 GCAGCAACTGTTTCTTCAGGTGGTTCTGTAGCCATGGCAGCAGTTATGGCTGGAGGAATG 15546
                                                                                                                                1213 GTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTGGTTGCAGCTCTG 1272
                                                                                 1273 TTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: doub
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les 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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Pred. No. 5.6;
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RESULT 5
US-09-676-610B-24
; Sequence 24, Application US/09676610B
parent No. 6444465
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CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 21;
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Best Local S
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51361 CGAGGTGGCCCTTGAGTGCCAAACAGCCTGTCCTCAGCTGCAAAATGAG 51409
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843 GAAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACT 902 AGAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAG 1011 TCAGATAATTAAGACAATTCATTCTCCTGAAACTGCTGTTCATGTAAAAAAGGAATTTTAT 51360 GTCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGT 962 l Similarity 85; Conser 1.4%; ilarity 50.3%; Conservative 0; Score 34.6; D: Pred. No. 33; O; Mismatches DB 4; 84; Length 169998; Indels 0; Gaps

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US-07-991-867B-25/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature; LOCATION: (25)..(1291); OTHER INFORMATION: WHerein any n is a, g, c, US-09-552-322-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/07991867B Patent No. 5476781
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/552,322 CURRENT FILING DATE: 2000-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gould-Rothberġ
APPLICANT: Rastelli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 15966-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Assembled OTHER INFORMATION: using sequences from AC024267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING ITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1896
                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION:
             CLASSIFICATION: 435
                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      FILING DATE:
                                                                   APPLICATION NUMBER:
                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                 COUNTRY: UZIP: 32606
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5, 6436642
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                                                                                                                                                                                                                                                                 E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                USA
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Hall, Richard L.
                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                          Floppy disk
                                                  12-DEC-1992
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WO 92/14818
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Pred. No. 2
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INFORMATION FOR SEQ ID NO:
                                 APPLICATION NUMBER: US 0 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 19-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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TOPOLOGY: unl
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REFERENCE/DOCKET NUMBER: UF114.C3
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                                                                                                                            APPLICATION NUMBER:
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Local Similarity 56.8%;
es 63; Conservat:...
   REGISTRATION NUMBER:
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nucleic acid
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                  Saliwanchik, David R
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Gruidl, Michael E.
WENTION: No. 5721352el Entomopoxvirus Expression System
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                                                                                                                                                                                                                                                                         IBM PC compatible
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Pred. No. 2.3;
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TELEPHONE:

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                  APPLICATION NUMBER: WO 92 FILING DATE: 12-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: double TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
            TELEPHONE: 904-375-8100
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                                                                                               FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                              NAME: Bencen, Gerard
REGISTRATION NUMBER:
                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 19-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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Local Similarity 56.8%;
                                                REFERENCE/DOCKET NUMBER:
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LICANT: Gruidl, Michael E.
LE OF INVENTION: No. 5935777el Entomopoxvirus Expression
BER OF SEQUENCES: 77
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2421 N.W. 41st Street, Suite A-1
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904-372-5800
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                                   RESULT 11
US-08-107-755A-1/c
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Sequence 1, Application US/08107755A Patent No. 5721352
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: P
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1992-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: UF114.C4.D1
                                                                                                                                                                                                                                                                                                                                            LENGTH: 1395
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: WO 92/14818 PRIOR FILING DATE: 1992-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1993-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/107,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1936: ATAGAGCCTGAATCTCAAACTTCTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
                                                                                                                                  1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
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                                                                                                             231 TTGGCTAGTAGTATAGAGGTGCATTATTTATTTCTAGATATGATATTAAT 181
                                                                                                                                                                                   291 ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 232
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                                                                                                                                                                                                                                                         Local Similarity
nes 63; Conser
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mes 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/657,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn version 3.1
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Pred. No. 2.3;
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Pred. No. 2.
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GENERAL INFORMATION:

APPLICANT: APPLICANT:

Moyer, Richard W. Hall, Richard L. Gruidl, Michael E.

TITLE OF INVENTION:

No. 5721352el Entomopoxvirus Expression System

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US-08-107-755A-1
                                                                                                                    Matches
                                                                                                                                  Query Match
Best Local Similarity
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                  1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
                                                                                     1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
                                                         355
                                                                                                                                                                                                                            FEATURE:
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LENGTH: 6768 base pairs
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PRIOR APPLICATION DATA:
07/827,658
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                                                                                                                                                                                                                                                                                                                                                                                                         EATURE:
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295 TTGGCTAGTAGTATAGAGGTGCATTATTTATTTCTAGATATGATATTAAT 245
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FILING DATE: 30-JAN-1992
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                                                         ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGAFTTA 296
                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (904)
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                         CDS
1474..2151
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2502..2987
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           complement (6277..6768)
                                                                                                                                                                                                                                      CDS
3080..6091
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Pred. No. 6.1;
                                                                                                                    Mismatches
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                                                                                                                                             DB 1;
                                                                                                                    48;
                                                                                                                                              Length 6768;
                                                                                                                  Indels
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RESULT 12

Best Local Similarity 56.1 Matches 63; Conservative

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Mismatches

48;

Indels

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Gaps

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US-07-991-867B-
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             Query Match
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                                                                                                                                  FEATURE
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LENGTH: 8457 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                       FEATURE
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APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CTTY: Gainesville
                                                                        NAME/KEY:
                                                                                                                   NAME/KEY:
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                                                           LOCATION:
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5. 5476781
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              904-372-5800
                                                                                                                                                CDS
2502.
                                                        CDS complement (6277..6768)
                                                                                                     CDS
3080..6091
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                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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1.4%;
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Score 34.2;
Pred. No. 7;
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             DB 1;
             Length 8457;
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55 A 55

355

1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA

. 1995

FEATURE:

ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 296

1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046

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US-08-544-332-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                   TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                 TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                             NAME/KEY:
                                                                          ORGANISM:
                                                                                                                           TOPOLOGY:
                                                                                                                                     STRANDEDNESS:
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NAME/KEY:
                             LOCATION:
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                                           CDS
                             complement (65..1459)
                                                                          Amsacta moorei entomopoxvirus
                                                                                                                        unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                  NFORMAL Gerard H. 35,746
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                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                              UMBER: US 07/657,584
19-FEB-1991
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US-09-370-861A-1/c
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Best Local S
Matches 63
                                                                                                                                                                                                                                                               SEQ ID NO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/370,861A CURRENT FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1992-02-12
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 07/991,867 PRIOR FILING DATE: 1992-12-07
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 07/657,584
                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1992-01-30
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: UF114.C4.D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                           LENGTH: 8457
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moyer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: No. 641022
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                                                                                             1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
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                             1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
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295
                                                              355 AFAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 296
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LOCATION:
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TTGGCTAGTAGTATAGAGGTGCATTATTTATTTCTAGATATGATATTAAT
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3080..6091
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2502..2987
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                                                                                                                                                                                                                                                                                                               1991
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                                                                                                                                             1.4%;
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Pred. No. 7;
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Pred. No. 7;
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RESULT 15 US-09-253-316-3/c ; Sequence 3, Application US/09253316

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NUMBER OF SEQ ID NOS: 34

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 1062

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate sequence
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Search completed: May 3, 2003, 20:11:34 Job time: 1035 secs
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: LOCATION: (1)...(1062)
; OTHER INFORMATION: n = A,T,C or G
US-09-253-316-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.8
watches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
ERRLIER FILING DATE: 1998-02-20
                                                                                                                                                                                              2179 GTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTC 2238
                                                                                                                                                                                                                                                                1999 GCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCC 2058
                                                                                                                  2239 ACCAAGTTCGGTTGAGTATACTGTTTTGCAT 2269
                                                                            591 NGCNGGCATNGTYTTRTANSWNGTNSWNARY 561
                                                                                                                                                              651
                                                                                                                                                                                                                                                                                                                       770 ARDATRTINSWRTCRCANGGYTGDATRTARCANARNCKYTTYTCYTTNCKCAT-YTCRCA 712
                                                                                                                                                                                                                                                                                                                                                                                                     830 GCYTTNSWNARYTGRAANGTNGGYTGRCANGTYTTNCCYTTNGGDATYTTDATNGTYTTN 771
                                                                                                                                                                                                                                        RTTNSWRTTYTCRTTNGTNACNCKRTTNSWDATNCCCATNCCRCANGTNCKNSWRCANGG 652
                                                                                                                                                          NGTCCAYTINGINGCYIGNACNARRCAYTIYTIYTICCADAINARNGGNARRIINCKRIA 592
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28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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Post-processing: Minimum Match 0%
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Perfect score:
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2581
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Q8YAV1
Q9FD62
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Q973B5
Q97UL6
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Q9KWF7
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Q93K31
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Q944G1
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Q89xw1 listeria mo
Q9fd62 enterococcu
Q9fd72 staphylococ
Q9fd83 staphylococ
Q9kwf7 kitasatospo
Q99w20 staphylococ
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Q973b5 sulfolobus
Q97ul6 sulfolobus
                                                                                           Q9fd67 enterococcu
Q93k31 lactobacill
                                                                                                                                                                           Description
                                                                                                                                                      Q9c6t1 arabidopsis
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Q9C6T1;

PRELIMINARY;

505 ₹

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.

core eudicots; Rosidae;

NCBI_TaxID=3702;

Hypothetical 54.4 kDa protein.

01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

 $\begin{array}{c} 117 \\ 128 \\ 138 \\$

ALIGNMENTS

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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Ra White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Ra Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., RA Baltarg S.L., Schwartz J.R., Shinn P., Southwick A.M., Shinn 
Nature 408:816-820(2000).
EMBL; AC079041; AAG50716.1; -.
TIGRFAMS; TIGR01219; Pmev_kin_ERG8; 1.
                                                                                                                  Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. COLUMBIA;
MEDLINE=21016719; PubMed=11130712;
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Q9fd77 staphylococ

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RESULT

Q944GLT

Q946GLT

ID 4GLT

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Query Match
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Matches 374
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Best Local
                                                                                                           STRAIN-CV. RRIM600;
Hallahan D.L., Keiper-Hrynko N.M.;
Hallahan D.L., Keiper-Hrynko N.M.;
"Genes involved in the biosynthesis of isopentenyl diphosphate rubber tree Hevea brasiliensis.";
submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP429385; AAL18926.1;
                                                                                                                                                                                                                                                                           Hevea brasiliensis (Para rubber tree).

Eukaryota; Viridiplantae; Etreptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids I; Malpighiales; Euphorbiaceae; Hevea.
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SEQUENCE 505 AA; 5
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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thes 374;
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                 Similarity
                                                                                                       TIGR01219;
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                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                74.8%;
74.1%;
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Score 1930.5; DB 1
Pred. No. 2.7e-140;
1; Mismatches 67;
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Pred. No. 1
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 52
                                TSPQ-LSRESMYKLSLN-----HLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKE
KSPQFINAEWLYNIDWTVSPIRVHQIYENCELEKNPNPFVQLALFYVI-NYFFSTGR---
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative phosphomevalonate kinase.
SPAC343.01C.
                                                                                                                                                              Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B. Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AL109739; CAB52264.1; -TIGRFAMS; TIGR01219; Pmev_kin_ERG8; 1.
                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=972H-;
                                                                                                                                                                                                                                                                            NCBI_TaxID=4896
                1 MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMN
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MKVTCSAPGKVLIAGGYIVLDPQYSGLVIGLTAKGYASTTTLDD
                                                                                 Similarity
                                                                                                                                 426
                                                                Conservative
                                                                                                                                 AA;
                                                                                                                                 47322 MW;
                                                                               19.1%;
                                                                               Score 493; DB 3;
Pred. No. 1.3e-29;
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                                                                  Mismatches
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Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res 8:123-140(2001).
EMBL; AP000984; BAB65998.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0973B5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ST0978.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-JCM 10545 / 7; PubMed=11572479;
                                                                                                                                                                                                                                InterPro; IPR001745; GHMPknse_ATP.
Pfam; PF00288; GHMP_kinases; 1.
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                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 314 AA; 35307 MW; 89740213AB16335F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfolobus tokodaii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
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37
                                 64
                                                                  w
                                                                                      6 SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAI--VKPINEEVKPESWAWKWTDVKLTSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETKLNDLSKLAKDHWDVYLRV--IKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLEL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV----AVTGLPLNEVIGTILKGK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QVHKTGLGSSAAMITSLIGSL--FLSLRRLTDDTGDKSLKIDDSTKVIVHNLAQI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --QPLCMQDLQVTLQVDNAYY-HQPQ------LKPDQ--TSYPKENFLNCTLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAP---FASITFNAAESNG 170
                            QLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITV-----EAKVDIEPLKQTNILDNIEQLPGVIGVGVPGAGGFDAQFCLAINHTEIIE 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSDV-VPFQLPATYCLLMGDV-AGGSSTPGMVKKVQQWQKENPEESK----NCFD-----
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                                                               SAPGKILWIGSYSVV-----
                                                                                                                                 113;
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                              9.1%; Score 235; DB 17; 23.2%; Pred. No. 6.3e-10; tive 64; Mismatches 129;
-----SSNNF-----IFETTYGTFKDK------
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                                                               -FGGISHVIAINKRVR------CDIK----
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                                                                                                                                                               Length 314;
                                                                                                                          Indels 182;
                                                                                                                            Gaps
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Qy	αu	Qy	Query M Best Lo Matches		RA Ch RA Ga RT "T RL Pr DR EM		RP SE		28	Db 3	Qy 4	Qy 4 Db 2	ОУ 3 Db 2	, 1		Qy 2 Db 1	Qy 1 Db	Db	0у 1
61 TSPQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119 : : : : : : : : : :	:	VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL 6	y Match 8.9%; Score 230; DB 17; Length 323; Local Similarity 22.2%; Pred. No. 1.6e-09; hes 110; Conservative 72; Mismatches 129; Indels 184; Gaps 21;	InterPro; IPR001174; Galkinase. InterPro; IPR001745; GHMPknse_ATP. Pfam; PF00288; GHMP_kinases; 1. PRINTS; PR00960; LMBPPROTEIN. Kinase; Complete proteome. Kinase; Complete proteome. SEQUENCE 323 AA; 36207 MW; D62E48552F5CBDF8 CRC64;	t M., Gaasterland T., Van der Oost J.; on Sulfolobus solfataricus 7840(2001)	STRAÎN-AȚCC 35092 / DSM 1617 / P2; MEDLINE-21332296; PubMed-11427726; She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.CY., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X., Thi-Nqoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus. NCBI_TaxID=2287; [1] SEQUENCE FROM N.A.	01-OCT-2001 (TrEMBLrel. 18, Created) 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-UN-2002 (TrEMBLrel. 21, Last annotation update) (phospho) mevalonate kinase, putative. SSO2988.	5 7UL6: PRELIMINARY; PRT; 323 AA.	08 -EGLRIEA 314	80 PHGVCLES 487	20 PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVLALLVRED 479 : :: :: :: :: : :: :: ::: : :: ::	360 DVYLKVIKSCSVLTSEKWVLHATEPINBAIIKELLBARBAMLKIRILMRQMGBAASVPLE 419		LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSD	244 SCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMN 299 	184 SSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDV 243 : : ::::::::::::::::::::::::::::::	54GNELIESVITVFKEKFGSLPPFHVKLFNDKDFQ-IHGKKTGLG 95	124 DITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGLG 183

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01-MAR-2001
01-JUN-2002
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EMBL; AF290093; AA602442.1; -...
TITHEREN. TERROL'S AA602442.1; -...
                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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MEDLINE=20353468; PubMed=10894743;
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                                              PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                                                                  IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
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-RRNGELVLDIR---
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s; TIGR01220; Pmev_kin_
                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                    368 AA;
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                    40541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487
                                                                                                                                                                                                                                  6.98;
                                                                                                                                                                                                                                                                                                                                                                     Pmev_kin_Gr_pos;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16, Created)16, Last sequence update)21, Last annotation updat
                                                                                                                                                                                                            58;
                                                                                                                                                                                                    Pred. No. 1.868; Mismatches
                                                                                                                                                                                                                               Score 178.5; DB 2
Pred. No. 1.8e-05;
--ENPF----HYVLAAIHL-TEKYAQEQNKEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                 390993D36577146D CRC64;
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                                                                                                                                                                                                                                                             DB 2;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                  Smeds A., Purtsi T., Palva A.; "Identification of a gene cluster Lactobacillus helveticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q93K31
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001745; GHMPknse_ATP.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2000) to the EMBL/GenBank/DDBJEMBL; AJ279018; CAC51372.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=53/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus helveticus
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                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                     Kinase
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416
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                                                                                                                                                                                             KYGLGSSAAVTVATVKAILHFYG-VKMSN--
                                                                                                                                                                                                                      KTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEALKNLCDLAESYTGA--AKSSGAGGGDCGIVIFRQKSGILPLMTAWEKUGITPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIAASCYGG--WIAFSTFDHDWVNQKVT----TETLTDLLAMDWPELMIFPLKVPKQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL
VPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGT-KLTQAWSSHNVLAL
                            -----NFLAASSEC-VLK----MIVGFKAKNIALIKKQIRVN----
                                                    KDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAAS
                                                                               DMKLMIG
                                                                                                          -MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKAR-ENWQNLSDANLELETKLNDLSKLA
                                                                                                                                     SAGDIAASVYGGWLAYQTFDKKWLQY-ELA-----NKTLSDVVNEAWPGLKIELLTPPH
                                                                                                                                                               SGFDVSCAVYGS-QRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL
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                                                                                                                                                                                                                                                 Similarity 24.8
75; Conservative
                                                                                                                                                                                                                                                                                                      294 AA;
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                                                                                                                                                                                                                                                                                                       32537 MW;
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Last annotation update)
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                                                                                                                                                                                                                                                 Score 158.5; DB 2;
Pred. No. 0.00045;
2; Mismatches 117;
                                                                                 -WSQKPASTSRLVDETNANKAALNTEYK-
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                                                                                                                                                                                                                                                                                                       0795099A1BC97938 CRC64;
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01-JUN-2002 (TrEMBLrel. 2
Phosphomevalonate kinase.
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Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001969; Aspprotease_site
InterPro; IPR001745; GHMPknse_ATP.
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EMBL; AB037666; BAB07792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takagi M., Kuzuyama T., Takahashi S.,
"A gene cluster for the mevalonate pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20353446; PubMed=10894721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=93372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces sp. (strain CL190).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain CL190."
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LMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVP-GAGGFDAIFAITLGDSGTKLT-
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                                                                                                                                                                            CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT
                                                                                                                                                                                                                                   NSKPEVAKTGLGSSAAMTTAVVAALLHYLGV-VDLSDPCKEGKFGCSDLDVIHMIAQTSH
                                                                                                                                                                                                                                                                                         KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA
                                                                                                                                                                                                                                                                                                                      GWRWHDGRLV-
                                                                                                                                                                                                                                                                                                                                             AWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKD
                                                                                                                                                                                                                                                                                                                                                                        IVRHAPGKLFVAGEYAVVDPGNPAILVAVDRHISVTVSDADADTGAADVVISSDLGPQAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAIEIPRLTQLIKIAEDFGGA--AKTSGAGNGDCGIVITDADTDVDALENEWRRNGILPL
                                                                                               R-RLPAPKGLTLEVGWTGEP
                                                                                                                         EFSLPPLMNLFL-----GEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELE
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                                                                   TKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRI
                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00959; MEVGALKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00141;
                                                                                                                                                   -PKGSGGDLAASTWGG--WIAYQAPDRAF----VLDLARRVGVDRTLKAPWPGHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR01220; Pmev_kin_Gr_pos; 1.
>S00141; ASP_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                        -RKFGLGSSGAVTVATVAAVAAFCGLELSTDERFRLAMLATAELD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%;
19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39281 MW;
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15,
21,
                                         -TTDCVRSAVTALESGD--DTSLLHEIRRARQELAR---
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                                                                                               ASTASLVS--
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155; DB 2; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A2908B333C694E6D CRC64;
                                                                                                                                                                                                                                                              -SAIETVGRLLGERGQKVPALTLSVSSRLHEDG--
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation update)
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pathway
                                                                                                                                                                                                                                                                                                                   -----VRDP--DDGQQARSALAHVV.---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacteridae;
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from
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vazquez-Boland J.-A., Voss H., Wehland J., Co "Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; B
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charbit A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaser P., Frangeul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CLIP 11262
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                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMs; TIGR01220; Pmev_kin_Gr_pos;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00288; GHMP_kinases;
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InterPro; IPR001745; GHMPknse_ATP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11679669;
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              MLQIETLEEPVPTFSVGWTGT-PVSTGKLVSQIHAFKQED---
                                        NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNI.SDANLELET
                                                                                            QTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWD
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                                                                                                                                                                                                                                    DGEHWTFT
                                                                                                                                                                                                                                                              ESWAWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLAT 108
                                                                                                                                                                                                                                                                                         PGKLYVAGEYAVVESGHTAILTAVN-RYITLTLEDSERNELWIPHYENPVSWPIGGELKP 72
                                                                                                                                                                                                                                                                                                                   PGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVK----
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360 AA; 40110 MW; OFFDD7B062B42584 CRC64;
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Berche P., Bloecker H., Brandt P., Chakraborty;
Chetouani F., Couve E., de Daruvar A., Dehoux P
Chetouani F., Couve E., Duchaud E., Durant L., Duss
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                           Score 151.5; DB Pred. No. 0.00210; Mismatches 1
                                                                                                                                                                                 ---TFLKSEGIELTPVKM-----
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fshi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Mordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00288; GHMP_kinases; TIGRFAMs; TIGR01220; Pmev_kir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser P., Frangeul L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nordsiek G., Novella S., de Padios B., reter
Remmel B., Rose M., Schlueter T., Simoes N.,
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QTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPRO01745; GHMPknse_ATP.
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Dominguez-Bernal G., Duchaud F
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39981 MW;
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20.5%;
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9981 MW; 15156C40BD997A1C CRC64;
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                                                                                                                         -TFLKSEGIELTPVKM
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on update)
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InterPro; IPR000515; BPD_transp.
InterPro; IPR001745; GHMPknse_ATP.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRNUTS; PR00959; MEVGALKINASE.
TIGRFAMS: TIGRN1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR01220; Pmev_kin_Gr_pos; 1. PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
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InterPro; IPR000515; BPD_trans
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MEDLINE=20353468; PubMed=10894743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Bacillus/Clostridium gr
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VSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL----
                                                                                                                                                                                                                                          ---RRNGELVLDIR-----
                                                   GSSGAVTVATVKALNVFYAL------NLSQLEIFKIAALAN--LAVQDNGSCGD
                                                                                               GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFD
                                                                                                                                                                                                                                                                                      PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                                                                                                                                                            LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL
                                                                                                                                                                                                                                                                                                                                     IEVSAPGKLYIAGEYAVVETGHPAVIAAVDQFVTVTVESARKVGSIQSAQYSGMPVRWT-
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D7 01-JU
D8 Phosp
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01-MAR-2001
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01-JUN-2002
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BMBL; AF290091; AAG02437.1; -
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InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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MEDLINE=20353468; PubMed=10894743;
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                                    DVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN 299
                                                                                                                                                                                                                                                                                                                                                                          PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
DIAVSVYSGWLAYSTFDHDWVK-QQMEETS---
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                                                                                                           LGSSAAVLVSVVKALNEFYG-LELSNL
                                                                                                                                                           LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 AA; 39886 MW; 608EBD4DF5774EC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TremBLrel 16, Created)
(TremBLrel 16, Last seq
(TremBLrel 21, Last ann
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19.8%; Pred. No. 0.0
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-- VNDVLEKNWPGLHIEPLQAPENME
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}	מט	7 .	Qγ	Db	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	Ma:	SQ	Z Z	DR	DR DR	DR DR	3 P. 2	3 급	RA A	R P	RN	888	88	G E	Dī	DT C	ID	n m	Db	Qy	Db	γQ	Db	Qy
250 THE THE TRACK THE TRACKS THE VENT GENERAL TRAVERS TO THE TRACKS THE TRACKS THE TRACKS THE TRACKS TO THE TRACKS THE TR	- PHFVSEVKKLK -		298 MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKD 357	65 G-DIAVSVYSGWLAYSTFDHEWVKH-QIEDTTVEEVLIKNWPGLHIEPLQAPEN	240 GFDVSCAYY-GSQRYVRFSPEVLSFAQVAYTGLPLNEVIGTILKGKWDNKRTE-FSLPPL 297	: : : : : : : :	LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHM	91YAKSCDIAMKHFHLTIDSNLDDSNGHK 117	TPESLGTLAPFASITFNAAESNGAN	48IHSKALHHNPVTFSRDEDSIVISDPHAAKQLNYVVTAIEIFEQ 90	YKLSLNHLTLQSVSASDSRNPFVEHAIQYA	2 IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRFVTATIEEATQYKGT 47	PNAGLVLSTNARFYAIVKPINEEV	ery Match 5.3%; Score 136.5; DB 2; Length 358; st Local Similarity 21.5%; Pred. No. 0.03; tches 103; Conservative 60; Mismatches 180; Indels 135; Gaps	SEQUENCE 358 AA; 40203 MW; 67EF432FA155FFE5 CRC64;	Tickrams; Tickotzzo; Fmev_kin_Gr_pos; i. Kinase.	PRO0959; MEVGALKINASE.	<pre>InterPro; IPR001459; Mev_gal_kin. Pfam; PF00288; GHMP_kinases; 1.</pre>	EMBL; AF290087; AAG02426.1; InterPro; IPR001745; GHMPknse_ATP.	inemyt diphosphare biosyminesis in glam positive coc 101. 182:4319-4327(2000).	action, evolution and essentiality of the mevalonate pat	E.I., Brown J.R., Bryant A.P., Chalker A.F., Holmes D.	SEQUENCE FROM N.A. MEDLINE-20353468; PubMed-10894743;	ä	or became the contraction of the contractions	micutos. Bacillus /Clostridium group. Bacilla]	homevalonate kinase.	1-MAR-2001 (TrEMBLrel. 16, Last se 1-JUN-2002 (TrEMBLrel. 21, Last an	R-2001 (TrEMBLrel. 16, Created)	95 95 95 96 96 97 97 97 97 97 97 97 97 97 97 97 97 97	13	296 ETDKLKKLCDVGEKHGGASKTSGAGGGDCGITIINKVIDKNII 338	419 EPESQTQLLDSTNSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL 472	248 GDFLDQSHACVESLIQAFKTNNIKGVQKMIRINRRIIQSMDNEASVEI 295	360 DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMROMGEAASVPI 418	219 VLIGWTGSPASS-PHLVSEVKRLK-SDPSFY 247	300 LFLGEPGSGGSSTPSMVGAVKKWOMSDPEKARENWONLSDANLELETKLNDLSKLAKDHW 359

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01-OCT-2000
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a gene cluster encoding mevalonate pathway from a terpenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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NCBI_TaxID=2064;
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                                                                                                                                                 HRRTWRGSPAYRRYVGATGELV-DAAVIALEDGDTEGLLRQVRRARHEMVR----LDDEVG
                                                                                                                                                                                                  SKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMG
                                                                                                                                                                                                                                                         LSPPRNLCLEVGWTGNPVSTT----
                                                                                                                                                                                                                                                                                                  FSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDL
                                                                                                                                                                                                                                                                                                                                                      ARIDPRGSGGDIATSTWGGWIAYR-APD----RDAVLDLTRRQGVDEALRAPWPGFSVR
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                                                                                                EAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTK----LTQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RKFGLGSSGAVTVATVSAVAAHCGL----ELTAEERF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GRSVPPLG----WSISSTLHEDG
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0288; GHMP_kinases; 1.
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                                                   ----ELTALCATAERAGAAKPSGAGGGDC--GTALLDAEARYDRSPLHRQW
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19.5%;
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Last sequence update)
Last annotation update)
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Kinase; Complete pro
Kinase; 358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP003131; BAB41781.1; -...
Interpro; IPR001745; GHMPKNSe_ATP.
Interpro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
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Cui L., Oguchi A., Aoki K.-I., Nagai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.aureus (strain Mu50), an MEDLINE=21311952; PubMed=11418146;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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AD3123	T17339	T19446	H82737	B84857	S28014	A55573	A69536	T51799	AC1922	F84545	T17285	S67655	D84767	S31714	S57160
conserved hypothet	hypothetical prote	hypothetical prote	malate oxidoreduct	hypothetical prote	outD protein - Erw	11beta-hydroxyster	mevalonate kinase	CLB1-like protein	two-component hybr	hypothetical prote	hypothetical prote	probable membrane	probable pre-mRNA	NAD+-protein ADP-r	sulfite reductase

ALIGNMENTS

C:Accession: C86443

C:Accession: C86443

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

C.A.; Li, J.H.; Li, Y.; Kowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712 A; Map position: 1 A;Cross-references: GB:AE005172; NID:g11136726; PIDN:AAG31307.1; GSPDB:GN00141 A; Molecule type: DNA A; Residues: 1-505 <STO> A;Status: preliminary C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 unknown protein [imported] - Arabidopsis thaliana Matches Query Match
Best Local Similarity Genetics: 301 FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD 241 241 181 181 121 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL Conservative 100.0%; Score 2581; DB 2; 100.0%; Pred. No. 3.8e-191; 0; Mismatches Length 505; Indels 0; Gaps 300 360 300 240 240 0

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RESULT
T38650
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A; Accession: T38650
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A; Residues: 1-426 <MUR>
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401
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NVIKTWKDDGVVPMDVSPAFDGLAVE
                                KLTQAWSSHNVLALLVREDPHGVCLE 486
                                                                                    IRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG--T
| : || | | | | | | | : : :
                                                                                                                                                                                                        WSDV-VPFQLPATYCLLMGDV-AGGSSTPGMVKKVQQWQKENPEESK----NCFD----
                                                                                                                                                                                                                                     WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMYGAVKKWQMSDPEKARENWQNLSDANLEL
                                                                                                                                                                                                                                                                        AHCSAQGKVGSGFDVGAATWGSCIYRRFDPKLIEQLLVPYDEQIKNINFSTELRKIVSKK
                                                                                                                                                                                                                                                                                              SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV----AVTGLPLNEVIGTILKGK
                                                                                                                                                                                                                                                                                                                                           ----QVHKTGLGSSAAMITSLIGSL--FLSLRRLIDDTGDKSLKIDDSTKVIVHNLAQI
                                                                                                                                                                                                                                                                                                                                                              ANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPC--KEGKFGCSDLDVIHMIAQT
                                                                                                                                                                                                                                                                                                                                                                                                                --QPLCWQDLQVTLQVDNAYY-HQPQ-----LKPDQ--TSYPKFNFLNCTLG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSPQ-LSRESMYKLSLN------HLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKE 113
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                                                                                                                                                                    ETKLNDLSKLAKDHWDVYLRV--IKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLR
                                                                  ITV-----EAKVD1EPLKQTNILDNIEQLPGVIGVGVPGAGGFDAQFCLAINHTEIIE
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30.2%;
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Pred. No. 4.2e-30;
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August 1997
426
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C;Accession: S57588; A39606
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphomevalonate kinase (EC 2.7.4.2) - yeast N;Alternate names: protein YM9959.02; protein C;Species: Saccharomyces cerevisiae C;Date: 19-oct-1995 #sequence_revision 03-Nov-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 11, 620-631, 1991
A; Title: Cloning and characterization of ERG8, an essential
A; Reference number: A39606; MUID:91117228; PMID:1846667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain R; Tsay, Y.H.; Robinson, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: phosphotransferase
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A;Residues: 1-212,'R',214-417,'PLMT',422,'D',424 <TSA>
A;Cross-references: EMBL:M63648; NID:g553127; PIDN:AAA34596.1; PID:g171479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPNMDDYCNRNLFVIDIFSDD--AYHSQEDS----VTEHRG-----NRRLSFHS
                                                                                                                                                                                                                                                                                                                                                                                                                          KESLHKLLLQGLDITTLGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDVKLTSPQLSRESMYKLSLNHLTLQS----VSASDSRNPFVEHAIQYAIAAAHLATEKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINE-----EVKPESWAWK---W
LRAQTANDKRFSKVQWLDVTQADWGVRKEK-DPET
                                   TKLTQAWSSH--NVLALLVREDPHGVCLESGDPRT 492
                                                                          VATIRRSFRKITKESGADIEPPVQTSLLDDCQTLKGVLTCLIPGAGGYDAIAVITKQDVD
                                                                                                                                                                                               LELETKLNDLSKLAKDHWDV%LRVIKSC -- SVLTSEKWVLHATEPINEAIIKELLEAREA
                                                                                                                                                                                                                                                                              ---WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN
                                                                                                                                                                                                                                                                                                                      QAQGKIGSGFDVAAAAYGSIRYRRFPPALIS-----NLP---DIGSATYGSKLAHLVD
                                                                                                                                                                                                                                                                                                                                                                                                     HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt MLRIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG}
                                                                                                                                                            SRFMDGLSKLDRLHETHDDYSDQIFESLERNDCTCQKY---
                                                                                                                                                                                                                                       EEDWNITIKSNHLPSGLTLWMGDI-KNGSETVKLVQKVKNWYDSHMPESLKIYTELDHAN
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Pred. No. 5.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIPS:YMR220w
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YMR220w
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D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species
                                                                                                         RESULT 5
AE1434
AE1434
C:Species: Listeria innocua (strain Cl C:Species: Listeria innocua (strain Cl C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C:Accession: AE1434
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                                                               R;Glaser, P.; Frangeul, L.; Buchrieser, C.; A
.; Dominguez-Bernal, G.; Duchaud, E.; Durand,
D.; Jones, L.M.; Karst, U.
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A; Residues: 1-323 <KUR>
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A; Accession: F90479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision
C;Accession: F90479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE006641; NID:g13816374; PIDN:AAK43093.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Phospho)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jong, I.; Jeffries, A.C.; Kozera, C.J.; rrett, R.A.; Ragan, M.A.; Sensen, C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                 --MNLFLGEPGSGGSSTPSMVGAVKKW-QMSDPEKARENWQNLSDANLELETKLNDLSKL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSPQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119
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                                                                                                                                                                                                                                                                                                                                                                                 -- AKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGE
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Pred. No. 5.3e
72; Mismatches
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                                                                          Amend, d, L.;
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                                                                           A.; Baquero,
Dussurget, O.;
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                                                                           Berche, P.;
Lian, K.D.;
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                 Η.;
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Fsihi, H.
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                 m, A.; Ma
Wehland,
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A;Cross-references: GB:NC_003210;
A;Experimental source: strain EGD-
C;Genetics:
A;Gene: lmo0012
                                                                          A; Molecule type:
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-FA;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AE1806
                                                                                                                                                                                            mevalonate kinases homolog lmo0012 [imported] - Listeria monccyt C;Species: Listeria monccytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change C;Accession: AE1806 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                    Science 294, 849-852,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain C; Genetics:
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A;Experimental source: strain Clipl1262
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A; Residues: 1-360 <GLA>
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A;Accession: AE1434
A;Status: preliminary
                  A;Status: preliminary
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAG-VPGAGGFDAIFAIT-LGDSGTKLTQ
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DNA
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20.7%;
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Pred.
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d, L.; Dussurget, O.;
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                                                                                                     vat, G.; Madueno,
Vazquez-Boland, J
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                                                                                                                                                                                                F.; Berche, P.;
; Entian, K.D.;
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PIDN:CAC98227.1;

PID:g16409371;

GSPDB:GN00177

Wehla Α.

A; Molecule type: DNA A; Residues: 1-358 < KURN A; Residues: 1-358 < KURN A; Residues: 1-358 < KURN A; Cross - references: GB:BA000018; PID:g13700484; PIDN:BAB41781.1; GSPDB:GN00149 A; Experimental source: strain N315 C; GenetLcs: A; Gene: mvaKZ Query Match Best Local Similarity 21.8%; Pred. No. 0.015; Matches 104; Conservative 59; Mismatches 181; Indels 133; Gaps 23; Matches 104; Conservative 59; Mismatches 181; Indels 133; Gaps 23; Qy 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 Qy 63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122 Qy 63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122 i; :: : : : : : : : :	C; Accession: B89828 R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Accession: B89828 A; Status: oral minery	AW 466 EW 340 Factor of the control of the co	287 NKRTEFSLPPLMNLFLGEPGSGSSTPSMYGAVKKWQMSDPEKARENWQNLSDANLELET	109 EKDKESLHKILLOGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAES 88	Query Match S.8%; Score 149.5; DB 2; Length 359; Best Local Similarity 20.5%; Pred. No. 0.001; Matches 99; Conservative 60; Mismatches 146; Indels 177; Gaps 20; Oy 8 PGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVK
Qy 121 QGLDITILGSNDFYSYRNQIESAG	Query Match 5.0%; Score 130; DB 2; Length 816; Best Local Similarity 19.0%; Pred. No. 0.13; Matches 106; Conservative 76; Mismatches 203; Indels 174; Gaps 21; Qy 68 ESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDXESI.HKL-LL 120 :	A;Accession: Tz1/13 A;Status: prellminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-816 <wtl> A;Cross-references: EMBL:Z81526; PIDN:CAB04264.1; GSPDB:GN00019; CESP:F33H2.2 A;Cross-references: clone F33H2 C;Genetics: A;Experimental source: clone F33H2 C;Genetics: A;Gene: CESP:F33H2.2 A;Map position: 1 A;Introns: 51/1; 101/3; 186/1; 270/3; 328/2; 380/3; 509/2; 751/2 C;Superfamily: Caenorhabditis elegans hypothetical protein F33H2.2</wtl>	RESULT 8 T21713 T21713 C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T21713 R;Cottage, A. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19463	Db 166 -DIAVSYYSGWLAYSTFDHEWVKH-QIEDTTVEEVLIKNWPGLHIEPLQAPENM 217 Qy 299 NLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDH 358 QY :	

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A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943; PMID:9403685
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A; Residues: 1-317 <K
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                                                                                                                                                                                         AVVAIGIVCGLFLIHNATNVVEKGEIFK----
                                                                                                                                                                                                                  AAMTTAVVAALL----HYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCL-----AQGKV
                                                                                                                                                                                                                                              --LSQNCFFNLEN----
                                                                                                                                                                                                                                                                                                                       SRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDI
                                                                                                                                                                                                                                                                                                                                                   SVPGNLLLMGEYTILEEKGLGLAIAINKRAFFSFK-
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    IEPE----SQTQLLDSTMSAEGVLLAGVPGAGGFD--AIFAITLGDSGTK 461
                            HRNSILDFILKCN-LEMKKLVLNASNS-KSALISSLRRAKELGLAIG---EAIGVSAALP
                                                    HWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMROMGEAASVP
                                                                                                         MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKD
                                                                                                                                      GSGYDIATSIFGG--
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18.3%;
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                                                                                                                                                                                                                                            -FAYDVYIDTSNFFFN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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                                                                                 MQGLQ -- AIKTTTSICEYNK ----
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Vugt,
B.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C;Accession: AI2447 #sequence_revision 14-Dec-2001 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa,
                                                                                             RESULT
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                                                                               protein all5137 [imported] -
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mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) c; pate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #te: C; Accession: S42088 R;Riou, C; Tourte, Y.; Lacroute, F.; Karst, F. submitted to the EMBL Data Library, February 1994 A; Description: Isolation and characterization of a cDN, A; Description: Isolation and characterization of a cDN, and charac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: \hat{A}TP; isoprenoid biosynthesis; phosphotransferase F;330-339/Region: ATP binding #status predicted F;352/Binding site: ATP (Lys) #status predicted
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A; Residues: 1-378 <RIO>
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                                                                              RIRILMROMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITIGDSGT
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Kuritz, T.; Sa: ; Takazawa, M.;

Sasamoto,

Yamada,

S.; Watanabe, , M.; Yasuda,

; Irigu Tabata

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R;Graef, E.; Caselmann, W.H.; Wells
Oncogene 9, 81-87, 1994
A;Title: Insertional activation of
                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-396 <SCH
A; Cross-references: GB: M88468; NID: g307197; PIDN: AAB59362.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:107743,
R; Graef, E.; Caselmann, W.H.; Wells, J.; Koshy, R.
                                                                                                                                                                                                                                                                                           mevalonate kinase (EC 2.7.1.36) - human

#;Alternate names: MK

G:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence_revision 18-Mar-1997 #text_change 11-Jun-1999

C:Accession: A42919; A58527
                                                                                                                                                                                                           A; Reference number: A; Accession: A42919
                                                                                                                                                                                                                     R;Schafer, B.L.; Bishop, R.W.; Kratunis, V.J.; Kalinowski, J. Biol. Chem. 267, 13229-13238, 1992
A;Title: Molecular cloning of human mevalonate kinase and A;Reference number: A42919; MUID:92317034; PMID:1377680
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A;Title: Complete Genomic
A;Reference number: AB1807
A;Accession: AI2447
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A; Residues: 1-721 < KUR>
                                                     A; Accession:
                                                                      A; Reference number: S42226;
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                     Molecule type: r
Residues: 1-396
   Cross-references:
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NID:g450345;
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NCBIP: 107744)
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C;Genetics:
A;Gene: GDB:MVK
A;Cross-references: GDB:134189; OMIM:251170
A;Cross-references: T2pter 12qter
Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: ATP; isoprenoid biosynthesis; phosphotransferase
F; 335-357/Region: ATP binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Note: this enzyme can also utilize GTP, C;Superfamily: mevalonate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Pathway: isoprenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the reversible phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357/Binding
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KQALTSCGFD-----CLE----TSIGAPGVSIH
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                               HNVLALLVREDPHGVCLESGDPRTTCITSGVSSIH
                                                                                            QMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSS
                                                                                                                              GEMGE-
                                                                                                                                                              NDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR
                                                                                                                                                                                                                         RTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKL
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                                                                                                                                                                                                                                                                                         SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNK 288
                                                                                                                                                                                                                                                                                                                         WSELPPGAGLGSSAAYSVCLAAALLTV--CEEIPNPLKDGDCVNRWTKEDLELINKWAFQ
                                                                                                                                                                                                                                                                                                                                                     -----KTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEG----KFGCSDLDVIHMIAQT
                                                                                                                                                                                                                                                                                                                                                                                                                     LDITILGSNDFYSYRNQIESAGLP---LTPESLGTLAPFASITFNAAESNGANSKPEVA- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNIGIKRAWDVA----RLQSLDTS----FLEQGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                              ----ALGVGHASLDQLCQVT-RARG-LHSKLTGAGGGGC--GITLLKPGLEQPEVEAT
                                                                                                                                                                                              -TNTKVP
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Pred. No. 0.
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RESULT 13

A;Cross-references: EMBL:X75311; NID:g450345; PIDN:CAA53059.1; C;Keywords: phosphotransferase E;1-157/Region: hepatitis B virus large surface antigen (fragme F;162-557/Region: human mevalonate kinase (fragment) A; Molecule type: mRNA A; Residues: 1-557 <GRA> A;Title: Insertional activation of mevalonate kinase by A;Reference number: S42226; MUID:94134441; PMID:8302606 A;Accession: S42226 Oncogene 9, 81-87, 1994 C;Species: hepatitis B virus, HBV
C;Date: 13-Jan-1995 #sequence_revision 17-Mar-1997
C;Accession: S42226 R; Graef, E.; Caselmann, hypothetical large surface antigen/mevalonate kinase (EC W.H.; Wells, virus large surface antigen (fragment) J.; Koshy, #text_change hepatitis 2.7.1.36) mutant fusion PID: 9450346 20-oct-2000 Œ virus DNA ä prot

3 VVASAPG : 5 VLASAPA 58 VKLTSPG : :	aka, T.; Kudoh, Y.; Yamamot Yamamot Yamamot Y.; Kudoh, Y.; Yamazaki, J.; Kushida organization of the genome of a hyper-th 344137; pMID:9679194 sequence not shown; translation not show D:g3236133; pIDN:BAA30737.1; pID:g3258054 interim accession for a sequence replaced interim accession for a sequence replaced core 116; DB 2; Length 335; core 116; DB 2; Length 335; md. No. 0.36; 124. Tradol 180. Cons	LAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR 408	Query Match Best Local Similarity 20.2%; Pred. No. 0.68; Best Local Similarity 20.2%; Pred. No. 0.68; Matches 104; Conservative 74; Mismatches 183; Indels 154; Gaps 22; Qy 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESNAWKWTDVKLTS 62
Qy 305 -PGSGGSSTPSMVGAVKKWQMSDPEKARENWQNL 337	QUETY MATCH 4.5%; SCOTE 115; DB 2; Length 816; Best Local Similarity 21.4%; Pred. No. 1.8; Best Local Similarity 21.4%; Pred. No. 1.8; Matches 94; Conservative 68; Mismatches 164; Indels 114; G: 92 FVEHAIQYAIAAHLATEKDKESLHKLLLQGLDITILGSNDFYSYRNQIE	es: Lactococcus lactis subsp. lactis es: Lactococcus lactis subsp. lactis es: Lactococcus lactis subsp. lactis 23-Mar-2001 #sequence_revision 23-Mar-2001 #in A: Wincker, P.; Mauger, S.; Jaillon, O.; Res. 11, 731-753, 2001 The complete genome sequence of the lactic is not number: A86625; MUID:21235186; PMID:1133 ence number: A86625; MUID:21235186; PMID:1133 es; preliminary ule type: DNA ule type: DNA ules: 1-816 <sto> references: GB:AE005176; PID:g12723546; PIDN imental source: strain IL1403 ics: Clpc clpc family: endopeptidase Clp ATP-binding chain</sto>	Qy 118 LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEV 177 Qy 118 LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEV 177 Qy 118 AKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAOTSHCLAQ 234 Qy 178 AKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAOTSHCLAQ 234 Qy 178 CHURSTAVAVAATIGAVSRLLG-LELSKEEIAKLGHKVELLVQ 155 Qy 235 GKVGSGFDVSCAVVGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE 291 Qy 236 GASGIDPTVSAVGGFLYYKOGKFEPLPFME

357 SPDEAIAILQGLREKFEDYHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAV 416 389SVPIEPES 422 389SVPIEPES 422 389SVPIEPES 422 417 KISVKNQQTKRLDLEKELTEAQEELSEAVIKLDIKASRTKEKAVEKIADKIYKFSVKEDK 476 423 QTQLLDSTMSAEGVLLAGVP 442 3 ::

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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112
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Match
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Gapop 10.0 , Gapext 0.5
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2581
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    3.77
3.77
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                                                                                                                                                                                                                                                                                                                                                                     Length DB
   475
698
1158
443
463
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2492
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714
854
1163
331
893
3432
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378
335
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287
287
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2884
710
  DHILMOUSE
FTSH_CAPAN
NXIA_MOUSE
YJSP_YEAST
ALT_BPT6
KIME_ARCFU
LDHA_BRARE
GALL_CANPA
GSOD_ERWCH
PPB_SERWA
DHILHUMAN
ALT_BPT2
RI14_HUMAN
ALT_BPT3
YDAW_ECOLI
YEAST
YDAW_ETOLI
CYAA_USTMA
DHIL_SHEBMA
DHIL_SHEBMA
DHIL_SHEBMA
DHIL_SHEBMA
DHIL_SHEBMA
DHIL_SHEBMA
DHILMOMN
ALT_BPT3
YDAW_ETOLI
YEAST
YDAW_ETOLI
CYAA_USTMA
DHIL_SHEBMA
DHIL_SHEBMA
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BRICC_CLOAB
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KIME_RAT
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KIME_ARATH
KIME_HUMAN
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                                                                                                                                                                                  Q38433 bacteriopha
O27995 archaeoglob
O9pvk5 brachydanio
O42821 candida par
  082150
Q9nri5
Q97fk1
Q9be24
Q92974
P27395
                                                                          P39104 saccharomy
P49606 ustilago ma
P51975 ovis aries
                                                                                                                               Q38424
P48552
                                                                                                                                                                                                                                                                                P16232 rattus norv
Q9v187 pyrococcus
                                                                                                                                                                                                                                                                                                                 Q03426 homo sapier O59291 pyrococcus
                                                                                                                                                                                                                                                                                                      Q9r008 mus musculu
                                                                                                                                                                                                                                                                                                                                    P46086
                                                                                                                                                                                                                                                                                                                                               P24521 saccharomyc
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2 bradyrhizob
0 nicotiana t
5 homo sapien
1 clostridium
4 macaca fasc
4 homo sapien
5 j genome po
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4 capsicum an
4 mus musculu
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                                                                                                                                                                                                                                                                                                               pyrococcus
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ERG8_YEAST
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	DPO1_RICFE	\vdash	922	3.6	92.5	4
	ECHA_PIG	_	763	3.6	93	44
	EF2_METTH	_	730	3.6	93	3
P31700 erwinia chi	GSPD_ERWCH	L	712	3.6	93	12
	XYNA_THESA	ᆫ	1157	3.6	93.5	Ë
	GAL1_CANAL	L	515	3.6	93.5	Ö
P19110 j genome po	POLG_JAEV5	_	3432	3.6	94	39
	DNBI_HSVEB	_	1209	3.6	94	88
P17632 rhodocyclu	MBHL_RHOGE	_	618	3.6	94	37
	NF1_MOUSE	_	2841	3.7	94.5	36
C78489 guillardia	IF2C_GUITH	<u>_</u>	735	3.7	94.5	5
P39668 bacillus su	YYXA_BACSU	_	400	3.7	94.5	34

ALIGNMENTS

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451 AA; 50455 MW; DB2B6	418 423 TANDKR -> PLMTKC	T 213 213 A ->	183 183 ATP	ND BIND 150 160 ATD (DOTENTIAL)	ctorol biomethodic Air Dinding; isopiene biosynchesis;	F, 1.	DEPORTHER DRONGOT - CHUMD KITARCES APD. 1	HICROINIO, DEC. P. FRCO.	SULUI SUUUR SUUR EKKO CIII SULUI SUUR SUUR SUUR SUUR SUUR SUUR SUUR SU		٠.	Mb3b48; AAA3459b.1;			requires a license agreement (See http://www.isb-sib.c	ified and this statement is not removed. Usage by and for commerc	ng as its content is in no	the European Bioinformatics Institute There are no restrictions on its	hatwagen the Gwiss Institute of Bioinformation and the EMBI outstation -	This GWIGG-DDOT patty is Convertable It is produced through a collaboration	SUBFAMILY	-i- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE	!- SUBCELLULAR LOCATION: Cytoplasmic.	-!- PATHWAY: SECOND STEP IN ISOPENTENYL DIPHOSPHATE FORMATION.	diphosphomevalonate.	-i- CATALYTIC ACTIVITY: ATP + (R)-5-phosphomevalonate = ADP + (R)-5-	-i- FINCTION: ERGS IS AN ESSENTIAL GENE	Submitted (.TIN-1995) to the EMRI/GenBank/DDBT databases.	Data drom Warlch C	STRAIN=S2880 / AB972:		MOI. Cell. Biol. 11:620-631(1991).	Saccharomyces cerevisiae that encodes phosphomevalonate kinase.";	"Cloning and characterization of ERG8, an essential gene of	Tsay Y.H., Robinson G.W.;	MEDLINE=9111728: PIDMPG=1846667:	CEDITENCE OF 1-404 FED N N	NCBI_TaxID=4932;	Saccharomycetales; Saccharomycetaceae; Saccharomyces.	<pre>Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;</pre>	Saccharomyces cerevisiae (Baker's yeast).	ERG8 OR YMR220W OR YM9959.02.	is-oun-zooz (kei, 41, masc ambocation update)	(Rel. 34,	(Rel. 21, Creat		ERG8 YEAST STANDARD: PRT: 451 AA.	ERG8 YEAST

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RESULT 2
KIME_ARATH
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                                                       MEDLINE-20252529; PubMed-10794536;
Lluch M.A., Masferrer A., Arro M., Boronat
"Molecular cloning and expression analysis
gene from Arabidopsis thaliana.";
Plant Mol. Biol. 42:365-376(2000).
                                                                                                                                             "Isolation and characterization of a cDNA encoding thaliana mevalonate kinase by genetic complementati Gene 148:293-297(1994).
                                                                                                                                                                                              STRAIN-cv. Landsberg erecta; TISSUE-Leaf; MEDLINE-95047438; PubMed-7958957; Riou C., Tourte Y., Lacroute F., Karst F.
                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last send
16-CCT-2001 (Rel. 40, Last and
Mevalonate kinase (EC 2.7.1.36)
                                                                                                                                                                                                                                                                                                                                                                                           KIME_ARATH P46086;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 LRAQTANDKRFSKVQWLDVTQADWGVRKEK-DPET
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  phosphomevalonate.
ENZYME REGULATION:
PYROPHOSPHATE (GPP)
                                            CATALYTIC ACTIVITY: ATP + (R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAQGKIGSGFDVAAAAYGSIRYRRFPPALIS-----NLP---DIGSATYGSKLAHLVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKLTQAWSSH - - NVLALLVREDPHGVCLESGDPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VATIRRSFRKITKESGADIEPPVQTSLLDDCQTLKGVLTCLIPGAGGYDAIAVITKQDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRFMDGLSKLDRLHETHDDYSDQIFESLERNDCTCQKY ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEDWNITIKSNHLPSGLTLWMGDI-KNGSETVKLVQKVKNWYDSHMPESLKIYTELDHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHC
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30.1%;
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       AND
                                                                                                                                                                                                                                                                               Brassicaceae; Arabidopsis
    ACTIVITY I
D FARNESYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 453.5; DB 1;
Pred. No. 1.8e-26;
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                                          (R)-mevalonate =
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    IS INHIBITED IN
L PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                    cDNA encoding Arabidopsis complementation in yeast
                                                                                                                                                                                                                                                                                                      Embryophyta;
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                 IN VITRO
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    (FPP)
                                                                                                                                                                                                                                                                                           Tracheophyta;
udicots; Rosidae;
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    GERANYL
T BIND
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ID KIME_H
AC Q03426
DT Q1-QCT
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DE Mevvalo
GN MVK.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                01-OCT-1993
15-JUN-2002
                                                                                                                            Q03426;
01-OCT-1993
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NP_BIND 141 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001745; GHMPknse_ATP.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
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                                                                                                                                                                                KIME_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPETITIVELY AT THE ATP-BINDING SITE ON THE ENCYME.
PACHMAY: CHOLESTEROL BIOSYNTHESIS, MEVALONATE CATABOLISM.
SUBCELLULAR ICCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
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                                                                                                                                                                                                                                                                                                                                                         RIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGT
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     (Human).
                                                                                                                                                                                   STANDARD;
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41, Last anno
(EC 2.7.1.36)
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                                                      Last sequence up Last annotation 2.7.1.36) (MK).
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B; Mismatches
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Pred. No. 0
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                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no rest
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"Organization of the mevalonate kinase (MYK) gene and identification of novel mutations causing mevalonic aciduria and hyperimmunoglobulinaemia D and periodic fever syndrome.";
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S-309; R-326 A
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MEDLINE-9925935; PubMed-10369261;

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Poll-The B.T.;

Mutations in MVK, encoding mevalonate kinase, cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99330561; PubMed=10401001;
Houten S.M., Romeijn G.J., Koster J., G.
Smit G.P.A., de Klerk J.B.C., Duran R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS MEVALONICACIDURIA ILE-243; PHE-264; PRO-265
MEDLINE-99347937; PubMed-10417275;
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Caruso U., Landrieu P., Kelley R.I., Kuis W., Poll-The
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I-377, AND VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94134441; PubMed=8302606; Graef E., Caselmann W.H., Wells J
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Mosleular cloning of human mevalonate kinase and identification
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J. Biol. Chem. 267:13229-13238(1992).
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                VARIANTS HIDS LEU-167; THR-268 AND ILE-377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and characterization of three novel missense mutations in mevalonate kinase cDNA causing mevalonic aciduria, a disorder of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS MEVALONICACIDURIA MET-310 AND THR-334
MEDLINE-21214738;
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                                                                                                              ns in the gene encoding
  fever syndrome.";
et. 22:178-181(1999).
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9:81-87(1994).
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                                       N-20; P-20; P-39;
AND I-377, VARIANT
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Gibson K.M., Tanaka R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:1523-1528(1999).
PubMed=11313769;
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MEVALONICACIDURIA
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de Jong J.G.N.,
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                                         L-150; L-167; R-202; Q-2
MEVALONICACIDURIA T-334,
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-20; F-264; T-268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.com/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/li
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Eur. J. Hum. Genet. 9:260-266(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.

DISEASE: DEFECTS IN MVK ARE THE CAUSE OF MEVALONICACIDURIA. IT IS AN ACCUMULATION OF MEVALONIC ACID WHICH CAUSE A VARIETY OF SYMPTOMS SUCH AS PSYCHOMOTOR RETARDATION, DYSMORPHIC FEATURES, CATARACTS, HEPATOSPLENOMEGALY, LYMPHADENOPATHY, ANEMIA, HYPOTONIA, MYOPATHY, AND ATAXIA.
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ENZYME REGULATION: FARNESYL- AND GERANYL-PYROPHOSPHATES COMPETITIVE INHIBITORS.
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van der Meer J.W.M., Grateau
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TIGREAMS; TIGATE GHAP EMBL; EMBL; EMBL; EMBL; EMBL; VARIANT VARIANT VARIANT InterPro; IPR001745; GHMPknse_ATP
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1. Genew; PIR; A42919; EMBL; EMBL; EMBL; EMBL; VARIANT VARIANT Peroxisome; Transferase; PRINTS; PR00959; MEVGALKINASE EMBL; AF217535; AAF82407 1; AF217528; AAF82407 1; AF217529; AAF82407 1; AF217530; AAF82407 1; AF217531; AAF82407 1; AF217532; AAF82407 1; AF217533; AAF82407 1; AF217533; AAF82407 1; 260920; X75311; X75311; AF217534; HGNC:7530; Disease 138 1 20 148 135 ; AAB59362.1; ; CAA53060.1; ; CAA53059.1; A42919 52 39 Kinase; Cholesterol biosynthesis; ATP-binding; 20 AAF82407 148 20 52 39 mutation; 20 mevalon_kin; KINASES_ATP; ALT_INIT JOINED.
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S -> L (IN HIDS).
/FTId=VAR_010959.
A -> T (IN HIDS). H -> P (IN HIDS AND /FTId=VAR_004022. L -> P (IN HIDS). /FTId=VAR_010956. Polymorphism ATP (BY SIMILE A -> T (IN HIDS) /FTId=VAR_010960 /FTId=VAR_010957 1. SIMILARITY). MEVALONICACIDURIA).

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                                                                                                                                                                                                                                                                                                                                              3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS
                                                                               GEMGE --
                                                                                                                                                                                                                                                              LDITILGSNDFYSYRNQIESAGLP---LTPESLGTLAPFASITFNAAESNGANSKPEVA-
KQALTSCGFD-
                 HNVLALLVREDPHGVCLESGDPRTTCITSGVSSIH
                                                                                                NDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR
                                                                                                                                                              GERMIHGN-PSGVDNAVSTWGG------ALRYHQGKISSLKRSPALQILL-----
                                                                                                                                                                                                                                                                                   PNIGIKRAWDVA----RLQSLDTS----FLEQGD---
                                                                                                                                                                                                                                                                                                                           LLVSAPGKVILHGEHAVVH-GKVALAVSLNLRTFLRLQPHSN--
                                                           QMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSS
                                                                                                                                         RTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKL
                                                                                                                                                                                SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNK
                                                                                                                                                                                                     WSELPPGAGLGSSAAYSVCLAAALLTV--CEEIPNPLKDGDCVNRWTKEDLELINKWAFQ
                                                                                                                                                                                                                        -----KTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEG----KFGCSDLDVIHMIAQT
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                                        ALGVGHASLDQLCQVT - RARG
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                                                                                                                       -RNTRALVAGVRNRLLKFPEIVAPLLTSIDAISLECERVL
-TSIGAPGVSIH
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/FTId=VAR_010961.
P -> L (IN HIDS).
                                                                                                                                                                                                                                                                                                                                                                          Score 117; DB 1;
Pred No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_009068.
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                                                                                ----APAPEQYLVLEELIDMNQHHLN-----
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380
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                                                                                                                                                                                                                                                                                                                                                                  183;
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                                        -GITLLKPGLEQPEVEAT
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Best Local S
Matches 102
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InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinasee; 1.
PRINTS; PR00959; MEVGALKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermophilic archaebacterium, Pyrococcus horiko
DNA Res. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: ATP + (R)-mevalonate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikosnii.
Archaea; Euryarchaeota;
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16-OCT-2001
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059291;
                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR00549; mevalon_kin; 1. PROSITE; PS00627; GHMP_KINASES_ATP; 1
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MVK OR PH1625.
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP000006; BAA30737.1; -
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                                                                                                                                                                                                                                      3 VVASAPGKVLMTGGY-LVLEKPNAGLVLSTNARFYAIVKPINE--EVKPESWAWKWTD--
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COFACTOR: MAGNESIUM (BY SIMILARITY).
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 GKVGSGFDVSCAVYGSQRYV---RFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE
                                               AKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMTAQTSH---CLAQ
                                                                                        ---VGIDVSI---
                                                                                                                LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEV
                                                                                                                                                                 VKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHK
                                                                                                                                                                                                            VLASAPAKVILFGEHSVVYGKP--AIASAIELRTY-VRAQFNDSGNIKIEAHDIXTPGLI
                                                                                                                                                  VSFSEDKIYFETDYGKAAEVLS:
                                                                                                                                                                                                                                                                 Similarity 21.9
                                -GLGSSAAVAVATIGAVSRLLG-LELS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires a license agreement
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                                                                                                                                                                                                                                                                                                                             335 AA;
                                                                                                                                                                                                                                                                                                                                       Kinase; ATP-binding; Magnesium;
111 121 ATP (POTENTIAL)
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40,
EC
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, Last sequence upo
, Last annotation of C 2.7.1.36) (MK).
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                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                 Score 116; DB
Pred. No. 0.22
60; Mismatches
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                                                                                        -TSQIPV----
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horikoshii OT3."; 3
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                                -EIAKLGHKVELLVQ
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                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                            InterPro; IPR001745; GHMPknse_ATP
InterPro; IPR001174; Galkinase.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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Mammalia; Eutheria;
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                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9R008;
                Peroxisome.
NP_BIND
                                              PRINTS; PR00959; MEVGALKINASE.
TIGREAMS; TIGR00549; mevalon_kin; 1.
PROSITE; PS00627; GHMP_KINASES_ATP;
                                                                                                                                            MGD; MGI:107624;
                                                                                                                                                                                                                                                                                                                                                                                                               isoprene biosynthesis."
Hum. Mol. Genet. 8:1523
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification and characterization of three novel missense mutations in mevalonate kinase cDNA causing mevalonic aciduria, a disorder of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
  SEQUENCE
                                      Fransierase;
                                                                         PRINTS; PR00960; LMBPPROTEIN.
PRINTS; PR00959; MEVGALKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exeropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                            COMPETITIVE INHIBITORS (BY SIMILARITY).
PATHWAY: CHOLESTEROL BIOSYNTHESIS, MEVALONATE
                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic a
                                                                                                                                                                                                                                                                                                                                                  phosphomevalonate.
ENZYME REGULATION: FARNESYL- AND GERANYL-PYROPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY BE A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY
                                                                                                                                                                                                                                                                                SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LP----IVVGYTGSTG-STKELVAMVRKRYEEMPE-----LVEPILEAMGKLVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDL
                                                                                                                                                          AF137598; AAF00700.1; -...
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   395
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                138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Klerk J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Romeijn
                                      Kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                         LOCATION: Cytoplasmic and peroxisomal.

BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                               8:1523-1528(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10401001;
                148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
  41877
                                    Cholesterol biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
2.7.1.36) (MK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OAUIVI, Koster J., GI.
ATP (POTENTIAL).
, 953DB1C89403A3F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                           (R)-mevalonate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                SITE IN CHOLESTEROL BIOSYNTHETIC
                                                   ᆫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray R.G.
R., Gibson
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                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                              There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                           ADP
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F.
                                    ATP-binding;
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                                                                                                                                                                                                                                                                                                                             CATABOLISM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae;
                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                            EMBL
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MBL outstation -
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RESULT
DHI1_RA
       PRESENTATION OF THE PRESEN
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Best Local
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SEQUENCE OF 1-40.
MEDLINE=86278718; Pul
Monder C., Shackletor
Iohan F., Lakshmi V.;
"The syndrome of appa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Last sequence update) 16-OCT 2001 (Rel. 40, Last annotation updat Corticosteroid 11-beta-dehydrogenase, isozy (11-beta-hydroxysteroid dehydrogenase 1) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHI1_RAT P16232;
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                                                                                                                                                                                 MEDLINE=92375101; PubMed=1508221;
Moisan M.P., Edwards C.R., Seckl
"Differential promoter usage by t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                          dehydrogenase ge
Mol. Endocrinol.
                                                                                                                                                                                                                              SEQUENCE OF 1-69 F
MEDLINE=92375101;
                                                                                                                                                                                                                                                                                                                       dehydrogenase
                                                                                                                                                                                                                                                                                                                                            Agarwal A.K., Monder C., Eckstein B., "Cloning and expression of rat cDNA e
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90037015; PubMed=2808402;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                          "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSD11B1 OR HSD11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
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                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ALGVGHNSLDQLCQVT-AAHG-LHSKLTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASI----TFNAAESNGANSKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IHGN-PSGVDNAVSTWGGA--LRFQQGTMS----SLKSLPSLQILLTNTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLVSAPGKVILHGEHAVVH-GKVALAAALNLRTFLLLRPQSN------GKVSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ
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                                                                                                                                                                                                                                                                                                  Chem.
                                              Shackleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
                                                                                                                                                                 gene.
                                                                                                                                                                                                                                                                                                264:18939-18943(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                     FROM N.A
    apparent mineralocorticoid
                                                                                                                                       6:1082-1087(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RSTKALVAAVRSRLTKFPEIVAPLLTSIDAISLECERVLGEM-
                                                                        PubMed=3460996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.4%;
                                                 C.H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                    by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113.5; DB 1; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                 Bradlow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAAPVPEQYLVLEELIDMNQHHLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                           J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -FLE--
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                                                                                                                                                                                      rat
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1) (11-beta-HSD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                 H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446
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                                                                                                                                                                                    beta-hydroxysteroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152;
       excess:
                                                 New
                                                                                                                                                                                                                                                                                                                                              corticosteroid
                                                 M.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Rat
       its association
                                                 Stoner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with 11 beta-dehydrogenase and 5 beta-reductase consequences for corticosteroid metabolism."; J. Clin. Endocrinol. Metab. 63:550-557(1986).
Pyrococcus
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                                       MVK OR
                                                                    Mevalonate kinase
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: ATP + (R)-mevalonate .
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PRINTS; PR00959; MEVGALKINASE.
TIGRFAMs; TIGR00549; mevalon_kin;
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InterPro; IPR001174; Galkinase.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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PROSITE; PS00627; GHMP_KINASES_ATP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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SUBUNIT: HOMODIMER (BY SIMILARITY).
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             GEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHN
                                                                                                                                                                                                                                                                                                         LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEV 177
                                                                                                                                                                                                                                                                                                                                                                                                                       VVASAPGKVLMTGGY-LVLEKPNAGLVLSTNARFYAIVKPINE--EVKPESWAWKWTD--
                                                                      SKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR-QM
                                                                                                     HLPFVELPIVVGYTGSSG-STKELVAMVRRRYEEMPE----
                                                                                                                                LPPLMNL -- FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDL
                                                                                                                                                              QG-ASSGIDPTVSAIGGFLYY-----
                                                                                                                                                                                         QGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFS
                                                                                                                                                                                                                       ---GLGSSAAVAVATIGAVSKLL-
                                                                                                                                                                                                                                                  AKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVI-HMIAQTSH---CLA
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BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE
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Pred. No. 0.
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                                                                                                                                                                                                                       -DLELSKEEIAKMGHKVELLV 154
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O1-AUG-1990 (Rel. 15, L
16-OCT-2001 (Rel. 40, L
Meyalonate kinase (EC 2
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                                                                                                                                                                                                                                                              Peroxisome.
                                                                                                                                                                                                                                                                             PRINTS; PR00959; MEVGALKINASE.
TIGRPAMS; TIGRO549; mevalon_kin; 1.
PROSITE; PS00627; GHMP_KINASES_ATP; 1.
Transferase; Kinase; Cholesterol biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M29472; AAA41588.1; -. PIR; A35629; A35629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
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levels in rat liver.";
levels in Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson G.W., Mosley S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90222132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration veen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal. DISEASE: MUTATION IN THE MEVALONATE KINASE GENE CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER
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                                                                                    VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
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PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
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                                                                                                                                                Similarity
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41987 MW;
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Sciurognathi; Muridae
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                                                                                                                                                                    DB 1;
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RESULT
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Oppermann U.C.T., Netter K.J., Maser E.;
"Cloning and primary structure of murine 11 dehydrogenase/microsomal carbonyl reductase."

T. Biochem. 227:202-208(1995).
                                                                  Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: CATALYZES REVERSIBLY THE CONVERSION OF CO
INACTIVE METABOLITE CORTISONE
-i- CATALYTIC ACTIVITY: An 11-beta-hydroxysteroid + NAD
oxosteroid + NADPH.
                                                                                                                                                                                                                                                                                                                           MEDLINE-95178382; PubMed=7873449;
Rajan V.; Chapman K.E., Lyons V., Jamieson P., Edwards C.R., Seckl J.R.;
"Cloning, segments-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Corticosteroid 11-beta-dehydrogenase, isozyme 1 (EC 1.1.1.146) (11-DH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHI1_MOUSE
P50172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                             "Cloning, sequencing and tissue-distribution of hydroxysteroid dehydrogenase-1 cDNA.";
J. Steroid Biochem. Mol. Biol. 52:141-147(1995)
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                           Voice M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSD11B1 OR HSD11
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                          TISSUE SPECIFICITY: SIMILARITY: BELONGS
                                                      SUBCELLULAR LOCATION: Microsomal.
              SDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLECERVLGEM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINE -- Alikelleare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKGKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SINKWAYEGERVIHGN-PSGVDNSVSTWGGA--LRYQQGKMS----SLKRLPALQILLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAESNGANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKE----GKFGCSDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDITILGSNDFYSYRNQIESAGLP---LTPESLGTLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNVGIKQVWDVA----TLQLLDTG----FLE---QGDVPAPTL---
                                                                                                                                                        OF 1-10 FROM N.A.
                FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse)
                                                                                                                                                                                                                                         TISSUE=Liver;
91; PubMed=7851387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALGVGHASLDQLCQVT-AAHG-LHSKLTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGSSAAYSVCVAAALL--TACEEVTNPLKDRGSIGSWPEEDLK
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                          WIDELY
                            To
                          EXPRESSED, F
SHORT-CHAIN
                                                                                                                                                                                                                                                                                                cDNA.";
52:141-147(1995).
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                                         HIGHEST EXPRESSION IN LIVER
                            DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                 beta-hydroxysteroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
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                                                                                  NADP(+)
                                                                                                              CORTISOL
                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
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01-NOV-1997 (Rel. 35, Last
15-JUN-2002 (Rel. 41, Last
Cell division protein ftsH
(EC 3.4.24.-) (Fragment)
 Houlne G., Sch
Submitted (AUG
-!- FUNCTION:
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01-NOV-1997
01-NOV-1997
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CONFLICT
CONFLICT
SEQUENCE
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                                                            Capsicum annuum (Bell pepper).
Eukaryota; Viridiplantae; Streptophyta; Embryopl
Spermatophyta; Magnoliophyta; eudicotyledons; co
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                  SEQUENCE FROM N.A.
                                                                                                             FTSH
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                                                     NCBI_TaxID=4072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:103562;
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                                                                                                                                                                                                                                        ---KSEVYYDKSPLTPILLGNPG
                                                                                                                                                                                                                                                                                    ISGIINAQASPK-----EECAL-
                                                                                                                                                                                                                                                                                                       IAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVI-GTILKG
                                                                                                                                                                                                                                                                                                                            IAPYSASKFALDGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKE
                                                                                                                                                                                                                                                                                                                                                                                          ---SNDFYSYRNQIE----
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pr00106; adh_short; 1.
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70; Conser
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, Schantz M.L., Schantz R.;
(AUG-1995) to the EMBL/GenBank/DDBJ
ION: SEEMS TO ACT AS AN ATP-DEPENDENT
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1; ADH_SHORT; 1.
NADP; Microsome;
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                                                                                                                                          sequence update)
annotation updat
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Pred. No. 0.55
99; Mismatches
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N -> D (IN REF
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                                                                                                                            chloroplast precursor
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                                                                                    Embryophyta;
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T ZINC METALLOPEPTIDASE
                                                               core eudicots;
e; Capsicum.
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                                                                                    Tracheophyta;
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Pfam; PF01434; Peptidase_M41;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell division; ATP-binding; Transmembrane; Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000642;
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COFACTOR: BINDS 1 ZIN
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                      LHKLLLQGLDITIL---GSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA
                        SGNSGVIVLAATNRPDVLDSALLRPGKFDRQVTVDRPDVAGRVRILQVHSRGKALAKDVD
                                             WDNK----RTEFSLPPLMNLFLGEPGSGGSST----PSMVGAVKKWQMSDPEKA-----
                                                                      GVGASRVRHLFENAKSKAPCIVFIDEIDAVGRQRGAGLGGGNDEREQTINQLL-TEMDGF
                                                                                             -YGSQRY--
                                                                                                                     KYTALGAK - - -
                                                                                                                                           KEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDV----
                                                                                                                                                                                                                                                                YSEF-LNAVKKGKVERVRFSKDGSALQ-LTAVDGRR--
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                                                                                                                                                                                                                                                                                                              APIASPP-----QVMEVEAPNPNTSNPLPFSQNLVLNAPKTQASPVSD--LPESTQWR
                                                                                                                                                                  PGGPGGLGGPMDFGRSKSKFQEVPETG
                                                                                                                                                                                          NSKP---
                                                                                                                                                                                                                IDILAMNGVDISVSEGEGGNGLFSVIGNL------LFPFIAFAGLFFLFRRSQGG
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RENWONLSDANLELETKLNDLSKLAKDH-WDVYLRVI-
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BY SIMILARITY.
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Radota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Hayashtyaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                             Submitted (JUN-1998) to the EMPLESSAUL. (1998) to the EMPLESSAULTION: NEURONAL CELL SUCELL RECOGNITION AND CELL
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Graveley B.R., Philipps D.L.;
"Sequencing of the neurexin g
submitted (MAY-2001) to the E
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"Differential seizure-induced
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15-JUN-2002 (Rel.
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SIMILARITY: CONTAINS AT LEAST 2 LAMININ G-LIKE DOMAINS
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SIMILARITY:
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pubMed=11217851;
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Rodentia;
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LL ADHESION. MAY MEDIATE INTRACELLULAR
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01-FEB-1996 (Rel. 33
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YJR137C OR J2126.
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Eukaryota; Fungi;
             Saccharomyces cerevisiae (Baker's
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Matches
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Best Local
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EMBL; AF387674; AAK70470.1; -
EMBL; AF387674; AAK70471.1; -
EMBL; AK017578; BAB30815.1; -
EMBL; AJ006802; CAA07257.1; -
HSSP; Q63373; 1C4R.
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or send a
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-45/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00397; SIROHAEM.
PROSITE; PS00365; NIR_SIR; 1.
Hypothetical protein; Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S.
HYPOTHETAL 1300 1300 IRON-SULFUR (4FE-4S) (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Pfam; PF03460; NIR_SIR_ferr; 2.
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InterPro; IPR005117; Nir_sir_fer.
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InterPro; IPR001226; Flavodoxin.
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NCBI_TaxID=4932;
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                                                                  MVGAVKKWQMSDPEKARENWQNLSDA-------
                                                                                                       VVLTNIGNVNDYGNVINTVISNINKKEPDN--
                                                                                                                                                                                               DLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSF------AQ
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                                                                                                                                                                                                                                                             TGLGSS----
                                                                                                                                                                                                                                                                                                                    DFYSYRNQIES----AGLPLTP-----ESLGT-LAPFASITFNAAESNGANSKPEVAK 179
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                                                                                                                                                                   -LEILPS-SYTKIAVLQG------VSKKSQSNEFQPFLLDFFGNFNELVSRNIEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
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ETKLNDLSKLAKDHWD--VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAR
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Pred. No. 8
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IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
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E34695088BA9FE94 CRC64;
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Transferase; Glycosyltransferase.
SEQUENCE 698 AA; 77947 MW; 1704DF87A75CD835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The ADP-ribosyltransferases (gpAlt) of bacteriophages T2, T4, and T6: sequencing of the genes and comparison of their products."; Virology 203:294-298(1994).
-i- FUNCTION: COMPONENT OF THE PHAGE HEAD; ADP-RIBOSYLATES ONE OF 2 ALPHA-SUBUNITS OF THE BACTERIAL RNA POLYMERASE.
-i- SUBCELLULAR LOCATION: THIS PROTEIN IS INJECTED FROM THE VIRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998
15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content.
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NAD--protein ADP-ribosyltransferase (EC 2.4.2.-)
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                                 272 PLNEVIGTILKGKWDNKRTEF------SLPPLMNLFLGEPGSGGSSTPSMVGAVK 320
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P-DEVWGEITKNAWNAAKTKFLKRMIYSFSGIGAGPMIDITIARDGS--KYTPSQKRGIR
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                                                                                                                                                                              PEVA------KTGLGSSAAMTTAV-----VAALLHY------LGVVDLSDPCKEG
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                                                                      ----VILNAIKNEPTTSIKCLEK-----
                                                                                                       KFGCSDLDVIHMIAQTS-HCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGL
                                                                                                                                            PATAPLIPEAEEMKLGINSLASKTKAAKIIAEGTANELHYDYKFFSKSEVNEVSEKIKD-
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95; Conser
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i- CATALYTIC ACTIVITY: ATP + (R)-mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
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16-OCT-2001 (Rel.
Mevalonate kinase
                                                                                                                                                                                 InterPro; IPR001745; GHMPknse_ATP.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
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                                                                             Transferase;
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PROSITE; PS00627; GHMP_KINASES_ATP; 1.
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SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY.
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2.7.1.36) (MK)
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                                                                                                            -i- SOBCE...
entities requires a or send an email to
                                                                            This
                                                                                                                                                   "Molecular evolution of vertebrate lactate dehydrogenas gene duplication.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
-i- CATALXTIC ACTIVITY: (S) lactate + NAD(+) = pyruvate
                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Creace,
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                        use by non-profit institutions as long as modified and this statement is not removed. U
                                                                between
                                                                                                                                                                                                        SEQUENCE FROM N.A.
TSOI S.C.-M., Li J.Y.,
                                                                                                                                                                                                                                                           Actinopterygii; Ne
Cyprinidae; Danio.
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Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                  the European Bioinformatics Institute.
                                                                                                     -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
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                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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            (See http://www.isb-sib.ch/announce/
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PRINTS; PR00086; LLDHDRGNASE.
PROSITE; P800064; L_LDH; 1.
Oxidoreductase; NAD; Glycolysis; Multigene family.
Oxidoreductase; NAD; Glycolysis; Multigene family.
OXIDORED 0 BY SIMILARITY.
ACT_SITE 192 192 ACCEPTS A PROTON DURING CATALYSIS (BY SIMILARITY).

**APPANICATION OF THE PROTON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001557; L_LD
InterPro; IPR001236; ldh.
Pfam; PF00056; ldh; 2.
Pfam; PF02866; ldh_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF067201; AAF02212.1; -. HSSP; P00339; 9LDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZFIN; ZDB-GENE-991026-5; ldha.
                                                                                                                                                                                                     303 VVHMTLKPEEEKQLVKSAETLWGV 326
                                                                                                                                                                                                                                                                                                       413 AASVPIEPESQTQLLDSTMSAEGV 436
                                                                                                                                                                                                                                                                                                                                                                                                     248 TSWAIGMSVADLCESILKN----MHKCHPVS-TLVKGMHGVNEEVFLSVPCILGNNGLTD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 VGEHGDSSVPVWSGVNVAGVSLQALNPDLGTDKDKEDWKSVH--KMVVDSAYEVIKLKGY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 VSNPVDILTYVAWKLSGLPRNRVIGS--GTNLDSARFRY----LMGEKLGIHPSSCHGWV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 -----EVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNLFLG-EPGS----- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 HCLAQG--KVGSGFDVSCAVYGSQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 GANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 KIVADKDYSVTANSKVVVVTAGARQQEGESRLNLVQRNVNIFKFIIPNIIKYSPNCILLV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 GPTNKVTVVGVGMVGMAAAVSILLKDLTDELALVDVMEDKLKGE--AMDLQHGSLFLKTH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GGSSTPSMVG---AVKKWQMSDP----EKARENWQNLSDANLELETKLNDLSKLAK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHWDVYLRVIKSC-SVLTSEKWVLHATEPINEAIIKELLEA-REAMLRIRILMRQMG--E 412
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GenCore version 5.1.4_p5_457,8 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
  372.5
178.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAVVASAPGKVLMTGGYLVL.....ESGDPRTTCITSGVSSIHLE 505
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                                                                                                                                                                                                                                                          IJ
                                                                                                                                                          ABB77505
AAU15094
AAY72679
                        AAB18130
AAU35063
AAB60859
AAB99728
ABB49817
AAB60881
AAG81912
                                                                                                                                                                                                                                                                                                                           SUMMARIES
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1725.425 Million cell updates/sec
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                                                                                                                                                                                                                                                     Description
                   Streptomyces sp. C
Listeria monocytog
Mevalonate pathway
                                                                                                                                                            Arabidopsis thalia
Protein encoded by
Candida albicans p
Mevalonate path
S. epidermidis
                                                                                                                 Pinus radiata phos
Enterococcus faeca
                                                                                         Mevalonate pathway
                                                                                                                                                                                                                                                                                                                                                                                            printed,
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45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
	105.5	105.5	105.5	106	106	106	108	108	108.5	108.5	108.5	109.5	112	112	114	115	115	115.5	116.5	117	123	123	123	123	123	123	123	123	•	•	•	•	142.5	
4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.4	4 .5	4.5							4 .8	4 . 8		•			٠	٠			
949	949	931	308	1087	1073	1056	492	492	1477	1477	1477	369	338	287	823	816	432	723	952	396	456	451	447	398	380	378	378	378	358	345	358	358	362	358
22	22	22	22	21	21	21	22	22	21	15	14	11	22	23	22	23	21	22	22	12	21	. 21	21	21	21	21	21	21	22	22	22	22	23	22
аам79633	ABB12315	AAM78649	AAM79592	AAG31892	AAG31893	AAG31894	ABG15375	ABG06982	AAB01848	AAR63506	AAR41728	AAR05738	AAB96178	AAO14408	ABB71484	ABB53952	AAY43633 .	AAM80073	AAM79089	AAR13720	AAG50072	AAG50073	AAG50074	AAG50089	AAG51423	AAG51424	AAG50090	AAG12901	AAB60882	AAU34358	AAU37273	æ	405	AAB60883
Human protein SEQ	Human protocadheri	Human protein SEQ	Human protein SEQ	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Novel human diagno			Haemophilus high m	ě	glyceraldehyde-3-p	Putative P. abyssi	teroi	Drosophila melanog	Lactococcus lactis	Amino acid sequenc	Human protein SEQ	Human protein SEQ	Human mevalonate k		Arabidopsis thalia		Arabidopsis thalia			Arabidopsis thalia	Arabidopsis thalia	hway	Staphylococcus aur	Staphylococcus aur	Mevalonate pathway	0	Mevalonate pathway

ALIGNMENTS

RESULT 1

ABB77505 standard; Protein; 505 AA.

Arabidopsis thaliana PMVK SEQ ID NO

29-JUL-2002 ABB77505;

(first entry)

New nucleic acid encoding plant phosphomevalonate kinase, useful for identifying modulators, potentially useful as herbicides and growth regulators $\dot{}$ WPI; 2002-445360/48 N-PSDB; ABL60244. growth regulator; enzyme. 22-NOV-2000; 2000DE-1057755. 23-MAY-2002. DE10057755-A1. Arabidopsis thaliana Thale cress; PMVK; phosphomevalonate kinase; plant; herbicide; Meissner R, 22-NOV-2000; 2000DE-1057755 (FARB) BAYER AG. Lechelt-Kunze C;

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AAU15094
ID AAU1
XX AAU1
AC AAU1
XX AAU1
XX AAU1
XX AAU1
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XY Gene
XX Gene
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Best Local S
Matches 505
                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid (I, ABL60244) that encodes plant phosphomevalonate kinase (PMVK, ABB77505), excluding the know fully defined partial sequences ABL60245-ABL60247. Plant PMVK, (I), constructs and host cells that contain (I) are used to identify age that bind to and/or modulate activity of PMVK, potentially useful a herbicides and growth regulators. (I) is also used for recombinant production of PMVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                  Gene
                                                                                                                                         Protein encoded by C.
                                                                                                                                                                          04-DEC-2001
               23-AUG-2001
                                           WO200160975-A2
                                                                     Candida albicans
                                                                                                                                                                                                                                 AAU15094 standard;
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                                                                                                  replacement
                                                                                                                 identification;
                                                                                                                                                                                                                                                                                                                         HGVCLESGDPRTTCITSGVSSIHLE 505
                                                                                                                                                                                                                                                                                                                                                                                                                        VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL
                                                                                                                                                                                                                                                                                                         HGVCLESGDPRTTCITSGVSSIHLE 505
                                                                                                                                                                                                                                                                                                                                                                ESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVLALLVREDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 100.0%; al Similarity 100.0%; 505; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505
                                                                                                                                                                         (first
                                                                                                  and
                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                       entry)
                                                                                                  essential gene; conditional exp
                                                                                                                                           albicans essential gene CaYMR220W (ERG8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2581; DB 23;
Pred. No. 1.7e-236;
; Mismatches 0;
                                                                                                                                                                                                                                  ₽
                                                                                                  expression;
                                                                                                                 GRACE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identifial essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus funigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAUI5053-AAUI5113 represent proteins encoded by C. albican
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes - \,
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Pred. No. 1.4e-36;
8; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is phosphomevalonate kinase (PMK; ERG8) protein m Candida albicans. The ERG8 protein is useful in an assay for nntifying compounds that inhibit phosphomevalonate kinase (PMK) ivity. These inhibitors are useful as anti-fungal agents. The ERG8 and protein are also useful as reagents for diagnosing C. albicans
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DB; AAD02791, AAD02792
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CYAQKKIGSGFDVATAIYGLIVYRRFQPALINDVFQVLESDP--EKFPTELKKLIESNWE
                                                CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK----GKWD
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ASTRAZENECA UK
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Pred. No. 4.3e-36;
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applications, manipulating isoprenoid pathways or isoprenoid composition may, for example, affect plant development, pest resistance, and the value of extractives (e.g. plnene and myrcene). The ubiquitous and varied roles of isoprenoids make the polynucleotides attractive targets

for biotechnical applications in

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fields.

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in genome mapping, in physical mapping and in positional cloning of genes. The polynuclectides and polypeptides are useful in forestry and agriculture for manipulation of isoprenoid metabolism, in medicine for therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and chemical processing industries involving isoprenoids. In plant

Claim 26; Page 159; 164pp; English.

agriculture for manipulation of isoprenoid metabolism New plant polynucleotides encoding polypeptides involved production and modification of isoprenoids, useful in fo

forestry -

and

'n

The present invention

polypeptides involved

describes plant polynucleotides encoding in the production and modification of isoprenoids, steroid compounds. The polynucleotides are used

such as terpenoid and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000
                                                                                                                                                                                                    N-PSDB; AAA69566
                                                                                                                                                                                                                                Havukkala IJ
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29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                   Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                      pinene;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus
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(FLET-) FLETCHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRIL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELET
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                                                                                                                                                                                                                                                                                                                                                                                                                                             radiata
                                                                                                                                                                                                                                                                                                                                                                                     myrcene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphomevalonate kinase protein SEQ ID
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99US-0146441.
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RESULT 5
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                  prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; antibiotic;
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                                                                                                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                             antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU35063 standard; Protein;
programmes.
                                                                                                                                                                                                                                                                                                                            Example
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27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                   polynucleotides for the identification and development biotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HILL HILLIH H: HILL HILL HILL HILLH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSPQLAKEATYKLSLKTLSLQNVASSSSNGNPFVEQAVQFAVAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSPQLSRESMYKLSLNHLTLQSVSASDSR-NPFVEHAIQYAIAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-611495/70
                                                                                                                                                                                                                                                                                                                       3; Seq ID No 10656; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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; antibacterial; drug
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2000US-207727P.
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Xu HH;
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     nucleic acid
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Pred. No. 2.5e
15; Mismatches
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design.
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No. 2.5e-27;
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  sequence
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  rational drug 
is also usefu
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  useful
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                  (SMIK )
                                                                                              22-JUN-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                            Mevalonate
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                                                                                                                                                                       22-JUN-2000; 2000WO-US17262
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sequences encoding them have cardiant, osteopathic and cytostatic activities. The genes are applicable in producing e.g. ubiquitone, vitamin K2 and carotenoids which can be used in the treatment of heart diseases, osteoporosis and cancer in drugs and health foods. The present sequence represents the orfC protein from the present invention.
                                                                                                                                                                                                 The sequence given in AAH44043 represents a DNA sequence isolated from Streptomyces sp. CL190, containing a 6798 base pairs ($1), which encode the whole enzyme necessary for functioning the mevalonate pathway. The sequence encodes protein sequences, designated orfa to E and hmgr, which are used in the mevalonate pathway. The proteins and polynucleotide
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(KUZU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetes-originated genes of enzymes participating in mevalonate pathway, applicable in producing e.g. ubiquitone, vitamin K2 and carctenoids for treatment of heart diseases, osteoporosis and cancer idenge and health food
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112 KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKP-----INEEVKPESW CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT --QAWSSHNVLAL TKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRI R-RLPAPKGLTLEVGWTGEP---EFSLPPLMNLFL----GEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELE NSKPEVAKTGLGSSAAMTTAVVAALLHYLGV-VDLSDPCKEGKFGCSDLDVIHMIAQTSH 230 AWKWTDVKLTSPOLSRESMYKLSLNHLTLOSVSASDSRNPFVEHAIQYAIAAAHLATEKD IVRHAPGKLFVAGEYAVVDPGNPAILVAVDRHISVTVSDADADTGAADVVISSDLGPQAV LMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVP-GAGGFDAIFAITLGDSGTKLT--LDDEVGLGIFTPKLTALCD---AAEAVGGAAKPSGAGGGDCGIALLDAEASRDITH --PKGSGGDLAASTWGG--WIAYQAPDRAF----VLDLARRVGVDRTLKAPWPGHSV --- RKFGLGSSGAVTVATVAAVAAFCGLELSTDERFRLAMLATAELD Conservative 474 -TTDCVRSAVTALESGD--DTSLLHEIRRARQELAR---68; Score 155; DB 2; Pred. No. le-05; 68; Mismatches 1; -ASTASLVS -SAIETVGRLLGERGQKVPALTLSVSSRLHEDG------VRDP--DDGQQARSALAHVV----172; -DLHRRTWRGSASHQRFVE Indels 156; Gaps 352 265 220 290 171 127 95 111 67 51 299 19;

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Chakraborty T, Doma...
Perez-Diaz J, Baquero F
Perez-Diaz De Pablos P
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
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                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytopens and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                          Sequence
                                                                                                                                                                                                                                 monocytogenes and related organisms.
                                                                                                                                                                                                                                                sequence and proteins encoded by it are useful in pharmaceutical vaccines compositions for the treatment or prevention of infective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB49817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB49817 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
13
                                   8
                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                   modulate L. monocytogenes-related diseases.
                                   PGKLYVAGEYAVVESGHTAILTAVN-RYITLTLEDSERNELWIPHYENPVSWPVGGELKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-010914/01
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID No 2522; 192pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                    5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                              Score 149.5; DB 23,
Pred. No. 3.1e-05;
"" smatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359
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                                                                                                     DB 23;
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                                                                    Indels
                                                                                                     Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treatment
                                                                  177;
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Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                Gaps
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 AAB60881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                         Brown JR, (
Wilding EI;
The present invention relates to an isolated mevalonate pathway gene derived from a bacterium from clade of Class II of the phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g.
                                                                                                                                                                                                                22-JUN-1999;
02-AUG-1999;
                                                           Claim
                                                                                 New isolated mevalonate bacterium is useful for
                                                                                                                    WPI; 2001-071392/08
                                                                                                                                                                             (SMIK )
                                                                                                                                                                                                                                                                                                                       Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                            Mevalonate pathway; disease;
                                                                                                                                                                                                                                                                                                                                                                     Mevalonate pathway protein
                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60881;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60881 standard; protein;
                                                                                                                                                                                                                                                 22-JUN-2000; 2000WO-US17262
                                                                                                                                                                                                                                                                           28-DEC-2000
                                                                                                                                                                                                                                                                                                 WO200078935-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAG-VPGAGGFDAIFAIT-LGDSGTKLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLQIETLEEPVPTFSVGWTGT-PVSTGKLVSQIHAFKQED----SKNYQHFL-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALSHLVVQGNGSCGDIASCMYGGWIAYTTFDQEWVKH-RLAYKSLE-----WFMKEPWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGANSKPEVAKTGLGSSAAMTTAVVAALL - - HYLGVVDLSDPCKEGKFGCSDLDVIHMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESWAWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLAT
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                                                           20; Page 33;
                                                                                                                                                                             SMITHKLINE BEECHAM SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340
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                                                                                                                                                      Gwynn M,
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                              99US-0140519
99US-0146682
                                                        158pp;
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                                                                                                                                                       Mathie TB,
                                                                                 pathway gene
treatment of
                                                         English
                                                                                                                                                                             CORP
PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                infection
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                                                                                                                                                       Myers
                                                                                 polynucleotide derived bacterial infection -
                                                                                                                                                       JE,
                                                                                                                                                        Traini
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RESULT 10
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                                                                                                                                                                                               Staphylococcus epidermidis vaccination; endocarditis.
                        Kimmerly WJ;
                                                                       09-NOV-1999;
                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                   epidermidis open reading
                                                                                                                                                                                                                                                           03-SEP-2001
WPI; 2001-316495/33
                                                                                                09-NOV-2000; 2000WO-US30782
                                                                                                                                               WO200134809-A2
                                                                                                                                                                                                                                                                                   AAG81912;
                                                                                                                                                                                                                                                                                                           AAG81912 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conjunctivitis,
                                                                                                                        17-MAY-2001.
                                                (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GSSGAVTVATVKALNVFYAL-------NLSQLEIFKIAALAN--LAVQDNGSCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ---RRNGELVLDIR------ENPF-----HYILAAIRL-TEKYAQEKNILL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL
                                                                                                                                                                                                                                                                                                                                                                                              AL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HWDVYLRVIKSCSVLTSEKWVLHATEPINEAI--IKE--LLEAREAMLRIRILMRQMGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAASCYGG--WIAFSTFDHPWLQEQETQHSISELLALDWPG-----LSIEPLIAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEVSAPGKLYIAGEYAVVETGHPAVIAAVDQFVTVTVESARKVGSIQSAQYSGMPVRWT-
                                                                                                                                                                                                                                                                                                                                                                                                                      TGVVIETPALNKLCNLAEQYEGA -- AKSSGAGGGDCGIVIVDQKSGILPLMSAWEKAEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
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                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SFYDLK-
                                                                         99US-0164258
                                                                                                                                                                      epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumonia, bacteremia and meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                         SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                 frame protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 147.5; DB 22,
Pred. No. 4.9e-05;
""smatches 171;
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                                                                                                                                                                                                                                   SEQ 'ID NO: 918
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AAB60883

AAB60883 standard;

protein; 358

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH55098 represent oligonucleotide sequences and primers which are use in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447 no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (II), given in AAG81434 to Announce.
(I) and (II) can have antibacterial activity and therefore can be a considered to produce the action of vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH52762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in vaccination. The nucleic acids (I) may be used to produce to sepidermidis polypeptides (II) via the production of vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 273; 2188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           182 LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                                                                                                                                                                                       DVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN
                                                                                                                              GDFLDQSHAC
                                                                                                                                                                                                        VLIGWTGSPASS-PHLVSEVKRLK-SDP-----
                                                                                                                                                                                                                                                                              DIAVSVYSGWLAYSTFDHDWVK-QQMEETS-----VNDVLEKNWPGLHIEPLQAPENME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQVKAPGKLYIAGEYAVTEPGYKSILIAVNRFVTATIEASNK-----VEGSIHS
                                                        ETDKLKKLCDVGEKHGGA--SKTSGAGG
                                                                                         EPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL 472
                                                                                                                                                                   DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMRQMGEAASVPI 418
                                                                                                                                                                                                                                                                                                                                                          LGSSAAVLVSVVKALNEFYG-LELSNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                ------FEQYVRSCNMNLKHFHL-----TIDSNLADNSG------QKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cor vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 19.8
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH53970 represent nucleic acids (I) encoding polypeptides in AAG81454 to AAG83120, from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%;
19.8%;
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                                                                                                                              VESLIQAFKTNNIKGVQKMIRINRRIIQSMDNEASVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142.5; DB 2
Pred. No. 0.00014;
2; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                          -----YIYKLAVIANMKLQSLSSCG-
                                                        -GDCGITIINKVIDKNII 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                              phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g. conjunctivitis, pneumonia, bacteremia and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an isolated mevalonate pathway derived from a bacterium from clade of Class II of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1999;
02-AUG-1999;
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 ETDKLKKLCDVGEKHGGA--SKTSGAGG
                                              GDFLDQSHAC
                                                                     DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMRQMGEAASVPI
                                                                                             VLIGWTGSPASS-PHLVSEVKRLK-SDP
                                                                                                                   LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                         DIAVSVYSGWLAYSTFDHDWVK-QQMEETS----VNDVLEKNWPGLHIEPLQAPENME
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                     EPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL
                                                                                                                                                                                        LGSSAAVLVSVVKALNEFYG-LELSNL---
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SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gwynn M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathway; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                           358 AA;
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99US-0146682
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                                              -VESLIQAFKTNNIKGVQKMIRINRRIIQSMDNEASVEI
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Pred. No. 0.00014;
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GDCGITIINKVIDKNII
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                                                                                                                                                                                                                                                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequence given in ABp35124 to ABp37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections particularly S. epidermidis infections. The sequences can be used to
                                                                                                                                                                                                                                                                                                                                           cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus antibacterial;
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                       screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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DVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN
                           LGSSAAVLVSVVKALNEFYG-LELSNL,-----YIYKLAVIANMKLQSLSSCG-
                                                      LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF
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                                                                                                                                                                PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
                                                                                                                                                                                              IQVKAPGKLYIAGEYAVTEPGYKSILIAVNRFVTATIEASNK
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an isolated mevalonate pathway gene derived from a bacterium from 60 Class II of the phylogenetic tree referred to in the specification. The invention manused for treatment of disease related to bacterial infection, e.g. conjunctivitis, pneumonia, bacteremia and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilding
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 17-18; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated bacterium is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1999;
02-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mevalonate pathway; disease; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001
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                                                                                                                                                                                 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDFLDQSHAC .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMRQMGEAASVPI 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAVSYYSGWLAYSTEDHDWVK-QQMEETS-----VNDVLEKNWPGLHIEPLQAPENME
                                                                             PQLSRESMYKLSLNHLTLQSVSASDS---RNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119
                                                                                                                                      IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRE--VTATIEEATQ-----YKGT-----
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LQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAK 179
                                           -----IHSKALHHNPVTFSRDEDSIVISDPHAAKQLNYVVTAIEIFEQ------
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                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mevalonate pathway gene polynucleotide derived useful for treatment of bacterial infection -
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99US-0146682
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                                                                                                                                                                                                                                                        5.3%;
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                                                                                                                                                                                                                                                        Score 136.5; DB 2
Pred. No. 0.00054;
                                                                                                                                                                                                                                  Mismatches
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RESULT 14
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                                                                                                                                                                                                                                                                      23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; antibiotic;
                                                                                                                                                           WPI; 2001-611495/70.
N-PSDB; AAS55132.
                                                                                                                                                                                               Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                       21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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                                                                                              Example 3; Seq ID No 12866; 511pp; English.
                                                                                                                                                                                                                                                             16-FEB
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                                                                                                                                                                                                                                    ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial;
                                                                                                                                                                                                                                                                                                                                                             2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Xu HH;
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invention is also useful

Pseudomonas

aeruginosa and

Enterococcus faecalis

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potential new targets

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the identification

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ARESULT 15
AAU34358
ID AAU34
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for antibiotic development. The antisense nucleic acids can also be use to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to scree for homologous nucleic acids which are required for cell proliferation a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
    21-MAR-2001; 2001WO-US09180
                                                                                                                              Staphylococcus
                                                                                                                                                                         antibiotic; antibacterial;
                                                                                                                                                                                             Antisense;
                                                                                                                                                                                                                                     Staphylococcus aureus cellular proliferation protein #634
                                                                                                                                                                                                                                                                                 14-FEB-2002
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                                            27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QYKGTIHSKALHHNPVTFSRD---EDSI--VISDPHAAKQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRF--VTATIEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETEKLKYLCDIAEKYHGA--SKTSGAGGGDCGITIINKDVDKEKIYDEWTKHGIKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGDFLEDSHRC----VEK-LIHAFKTNNIKGVQKMVRQN-----RTIIQRMDKEATVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLIGWTGSPASS-PHFVSEVKRLK-SDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDH
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                                                                                                                                                                      prokaryotic cellular proliferation
; antibacterial; drug design.
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essentify genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiel, pneumoniae, Pseudomonas aeruginosa and Entercoccus faecalis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for antibiotic development. The antisense nucleic acids can also be us to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The proteins can be used to screen compounds in rational drug
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16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDIT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
LRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEPES
                                                                                                                                                                                                                                                                                                                                       SAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVS
                                                                                                         GEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVY
                                                                                                                                                                                VSVYSGWLAYSTFDHEWVKH-QIEDT---
                                                                                                                                                                                                                                   CAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMNLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                              ILGSNDFYSYRNQIESA--GLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGLGS
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                                                                              GWTGSPASS-PHFVSEVKRLK-SDP-
                                                                                                                                                                                                                                                                                         SAAVLVSVIKVLNEFYDM------KLSNL-YIYKLAVIANMKLQSLSSCG-DIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QYKGTIHSKALHHNPVTFSRD---EDSI--VISDPHAAKQ------LNYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq ID No 5854; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 AA;
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r the identification of potential new targets The antisense nucleic acids can also be used
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Pred. No. 0.00098;
7; Mismatches 173;
                                                                                                                                                                                  -TVEEVLIKNWPGLHIEPLQAPENMEVLI
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                                                                                 ---SFYGDF
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423 QTQLLDSTMSAEGVLLAGVPGAGGEDAIFAITLGD-SGTKLTQAWSSHNV 471
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4: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-030-682-4

US-08-302-832-4

US-08-30-198-4

2 US-08-469-880-4

2 US-08-617-697-4

2 US-08-719-641-4

US-09-206-942-71

1 US-09-206-942-71

1 US-09-651-200-6

1 US-09-562-377-49

1 US-08-87-375-891A-4

1 US-08-87-375-891A-4

1 US-08-288-303-11

1 US-08-281-288-3

1 US-08-261-822A-3

1 US-08-261-822A-3

1 US-08-315-793-52
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US-09-134-001C-5355
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5355, Application Patent No. 6380370
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ALIGNMENTS

US/09134001C

TO STAPHYLOCOCC

	251	Db 223 VLIGWTGSPASS-PHLVSEVKRLK-SDPSFY	
	359	QY 300 LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW 359	
	222	Db 170 DIAVSVYSGWLAYSTFDHDWVK-QQMEETSVNDVLEKNWPGLHIEPLQAPENME	D
	299	Qy 242 DVSCAVY-GSQRYVRESPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN 299	ю.
	169	Db 124 LGSSAAVLVSVVKALNEFYG-LELSNLYIYKLAVIANMKLQSLSSCG-	D
	241	QY 182 LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF 241	0
	123	Db 92FEQYVRSCNMNLKHFHLTIDSNLADNSGQKYG 123	
	181	Oy 122 GLDITTIGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTG 181	2
	91	Db 55 KTLHYEPVKFDRNEDRIEISDVQAAKQLKYVVTAIEV	
	121	OY 63 PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121	
	54	EPGYKSILIAVNREVTATIEASNKVEGSIHS	
	62	Qy 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAMKWTDVKLTS	0
20;	Gaps 2	Query Match 5.5%; Score 142.5; DB 4; Length 362; Best Local Similarity 19.8%; Pred. No. 3e-06; Matches 94; Conservative 72; Mismatches 167; Indels 141; Ga	
		US-09-134-001C-5355	c,
		; ORGANISM: Staphylococcus epidermidis	
		; LENGTH: 362	`.
		5	
		; NUMBER OF SEQ ID NOS: 5674	
		; PRIOR APPLICATION NUMBER: US 60/055,779	
		FILING DATE: 1997-11-08	
		; FRIOR AFFLICATION NUMBER: ON OU/OO4, 904	_

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RESULT 2
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TITLE OF INVENTION:
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                                            Sequence 8, Application Patent No. 6284506 GENERAL INFORMATION:
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APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CURRENT APPLICATION NUMBER: US/07/475,577
APPLICATION NUMBER: US/07/475,577
FILING DATE: 06-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 LDITILGSNDFYSYRNQIESAGLP---LTPESLGTLAPFASITFNAAESNGANSKPEVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
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; ORGANISM: Phaffia rhodozyma
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                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                         TITLE OF INVENTION: HIGHLE OF INVENTION: OF NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                         STREET: 2001 Jeff
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                           COUNTRY: U.S.A. ZIP: 22202-0286
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                                                                                                                                        2001 Jefferson
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                                                                                                                                          Shoemaker and Mattare, Ltd
01 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                             OF NON-TYPEABLE
8
                                                                                                                                                                                                                         III, JOSEPH W
HIGH MOLECULAR WEIGHT SURFACE
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HAEMOPHILUS

PROTEINS

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TITLE OF INVENTION: ISOPRENOID PRODUCTION
FILE REFERENCE: ISOPRENOID PRODUCTION
CURRENT APPLICATION NUMBER: US/09/306,595C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 98108210
PRIOR FILING DATE: 1998-05-06
ONUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                           231 GGMEAIKSFTSIRFLITDSRIGRDTRSLVAGVNARLIQEPEVIVPLLEAIQQIADEAIRC
                                                                                                                                                                                                                                                                                                                                                               232 LAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE
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KPFELRTKLTGAGGGGCAVTLVPDDFSTETLQALMETLVQSSFAPYIARVGGSGVGF
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                                                REAMLRIRILMRQMGEAASVPIEPESQTQLLDSTM----SAEGVLLAGVPGAG-GF 447
                                                                                                                                                      LSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEA 396
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ilarity 21.6%;
Conservative 6
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Pred. No. 0.0032;
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                                                                                                        HAHLAALGVSHPSLEEIIR-IGAD 335
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                                                                                                                                                                                       Sequence 4, Application US/08302832 Patent No. 5603938
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APPLICANT: Barenk
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INFORMATION FOR SEQ
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-810
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                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                  TITLE OF INVENTION:
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    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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VENTION: High Molecular Weight Su
VENTION: of No. 5603938-Typeable
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LENGTH: 1477 amino acids
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Local Similarity 20.38;
es 89; Conservative
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REGISTRATION NUMBER: 22,651
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Sequence 4, Application US/08530198 Patent No. 5869065

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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364 RVIKSCSVLTSEKWVLHA 381
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                                                              312 TPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLND--LSKLAKDHWDV-----YL 363
                                                                                                                                                                                             212 GKFGCSDLDVIHMTAQT----SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JW
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                                                                                              AKTGGFVETSGHDLFIKDNAIVDA---KEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG
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Best Local Similarity 20.3
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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305 EGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLG----GDERGE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REGISTRATION NUMBER: 22,651
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    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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High Molecular Weight Surface Proteins
of No. 5876733-Typeable Haemophilus
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Query Match 4.2%; Score 108.5; DB 2; Length 1477; Best Local Similarity 20.3%; Pred. no. 0.13; Matches 89; Conservative 68; Mismatches 162; Indels 119; Gaps 21; Qy 11 VLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWT	LENGTH: 1477 amino acids TYPE: amino acids TYPE: amino acid TYPE: single TYPE: TOPOLOGY: linear US-08-728-470-4	TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEPAX: (703) 415-0813 INFORMATION FOR SEQ ID NO: 4: SECURENCE CHARACTERISTICS.	GB 9205704. 1992 ION: Jerry W 22,651	CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION TOWN	AARIE 1	Patent No. 5928651 GENERAL INFORMATION: APPLICANT: Barenkamp, Stephen J APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd. STREET: Bldg. 1 CITY: Arlington STATE: Virginia	Db 507 TVNSSINIGSNSHLILHS 524 RESULT 8 US-08-728-470-4 ; Sequence 4, Application US/08728470	Qy 212 GKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRESPEVLSFAQV 266
TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEPHONE: (703) 415-0813 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1477 amino acids	` T : 3 P	; FILING DATE: 01-APR-1996 ; CLASSIFICATION: 424 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/302,832 ; FILING DATE: 05-OCT-1994 ; PRIOR APPLICATION NAMEA:	COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS COFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697	JOI Jefferson Davis Hwy. ldg. 1 rightin rightin J.S.A. 2-0286 RABLE FORM:	617 encencencent ITLITLITLITLITLITLITLITLITLITLITLITLITLI	Db 412 AKTGGEVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDERPTGTG 468 Qy 312 TPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVYL 363	OY 212 GKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV 266	Db 139 ILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIV 198 Qy 57DVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIA 102 Qy 57

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                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/302,832
                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                PRIOR APPLICATION DATA:
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                               APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                               FILING DATE
                                                                                                                                                            OPERATING SYSTEM:
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STRANDEDNESS: si
 APPLICATION
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                                                                                                                                                                                                        Sequence 71, Application US/09206942 Patent No. 6432669
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                                                 CURRENT APPLICATION NUMBER: U$/09/206,942
CURRENT FILING DATE: 1998-12-08
                                                                                                 TITLE OF INVENTION: Protective Recombinant Haemophilus TITLE OF INVENTION: Molecular Weight Proteins
                                                                                     FILE REFERENCE: 1038-861 MIS:jb
                                                                                                                                   APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel
NUMBER
                 EARLIER FILING DATE: 1998-10-07
                               EARLIER APPLICATION NUMBER: 09/167,568
                                                                                                                                                                      APPLICANT: Loosmore, Sheena
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LENGTH: 1477
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                                                                                                                                              SEQ ID NO 4
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   Matches
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                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/651,200 CURRENT FILING DATE: 2000-08-30 PRIOR APPLICATION NUMBER: 60/152383
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 15966-562 (CURA-62)
                                                                                                                                                                 SOFTWARE:
                                                                                      LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens
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y Match
4:0%; Score 104.5; DE
Local Similarity 22.3%; Pred. No. 0.042;
nes 87; Conservative 45; Mismatches 1
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                                                                                                                                                                                                                                       APPLICATION NUMBER: 1999-
                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKITISDIINP----TITYSIA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIV 198
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                                                                                                                                                                   Ver.
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Pred. No. 0.13;
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                                   DB 4;
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TELEFAX: (619) 235-017 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

LENGTH:

amino acid

770 amino acids

TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550

235-0176

REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:

29,655

DESMOS.002CP2

Israelsen, Ned A.

NAME:

MOLECULE TYPE: HYPOTHETICAL:

TOPOLOGY: STRANDEDNESS:

linear . protein NO

single

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US-08-445-135-2
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Patent No. 5658789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICATION NUMBER: US 01 FILING DATE: 12-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                         CLASSIFICATION: PRIOR APPLICATION
                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                               FILING DATE
                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --MSAEGVLLAG-----VPGAGGFD--AIFAITLGDSGTKLTQAWSSHNVLALLVR-- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEV 301
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                                                           DATA:
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                                      US 08/151,134
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09651200 Patent No. 6429303
                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                             FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                    APPLICANT: Green et al TITLE OF INVENTION: Polynucleotides Encoding Members of the Human TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 15966-562 (CURA-62)
                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                               PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-09-03
                                     TYPE: PRT
                                                     ENGTH:
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CLONE: 150 kD
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 GSGGSSTPSMV---GAVKKWQMSDPEKARENWQNL-----SDANLELETKLNDLSK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 RESM--YKLSLNHL--TLQSVSASDSRNPFVEHATQYATAAAHLATEKDKESLHKLLLQG 122
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                                                       534
                                                                                           PatentIn Ver. 2.0
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19.1%; Pred. No. 0.
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                                                                                                                                         ; OTHER INFORMATION: Description of Unknown Organism: OTHER INFORMATION: mz5020.protein from Figure 4. US-09-651-200-24
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                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-09
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-12
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-02
                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09651200 Patent No. 6429303
                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651
CURRENT FILING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                   LENGTH: 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 GSSAAMTTAVVAALLHY-----LGVVDLSDPCKEGKFGC------SDLDVIHMI 225
                                 183 GSSAAMTTAVVAALLHY-----LGVVDLSDPCKEGKFGC------SDLDVIHMI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 YSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 EDPVVALVG----TDATLRCSFSPEPGFSLAQ-----LNLIWQ---LTDTKQLVHSFTE
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98
                                                                    Local Similarity les 97; Conserv
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GSAYANRTALFPDLLAQGNASLRLQRVRVAD---EGSFTCFVSIRDFGSAAVSLQVAAPY 142
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97; Conserv
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48; Mismatches
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    YSCLVRNPVLQQDAHGSVTITGQPMTFPPEALW 468

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Qy	226	226 AQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK 282	
Вb	143	143 SKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDG-QGVPLTGNVTT 192	
Qy	283	283 GKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQM 324	
Db	193	193 SQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVTITPQRSPTGAVEVQVP 252	
Qy	325	SDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHA-TE 383	
Db	253	253 EDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTE 299	
Qy	384	384 PINEAIIKELLEAREAMLRIRILMROMGEAA 414	
망	300	300 GRDOGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCEVSIRDFGSAAVSLQVAAP 359	
Qy	415	415SVPIEPESQTQLLDSTWSAEGVLLAGVPGAGG 446	
Db	360	360 YSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGL 419	
Qy	447	TQAWSS	
Ъ	420	420 FDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEALW 468	
Qy	495	ITSGVS 500	
В	469	469 VTVGLS 474	

Search completed: April 26, 2003, 12:57:54 Job time : 22 secs

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Minimum
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Gapop 10.0 , Gapext 0.5
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Match
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US-09-909-745-22
US-09-909-745-24
US-09-909-745-16
US-09-909-745-18
US-09-909-745-18
US-09-9815-242-10656
US-09-815-242-12866
US-09-815-242-5854
US-09-909-745-23
US-09-909-745-23
                                                                                           US-09-925-388-8
US-10-092-880-4
US-10-077-023-7
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US-09-875-338-9
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Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 13670, A
Sequence 9, Appli
Sequence 9, Appli
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sequence 22, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 10656, A
Sequence 12866, A
Sequence 5854, Appl
Sequence 23, Appl
                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-988-863A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-988-863A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09988863A
Patent No. US20020123427A1
GENERAL INFORMATION:
APPLICANT: Bayer AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Plant phosphomevalonate kinases FILE REFERENCE: Le A 35 018 CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21
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2344 633	551	3313	1173	794	7968	1165	551	1386	730	714	679	1176	532	385	948	640	514	806	387	492	1599	854	657	863
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US-09-815-242-12713 US-09-815-242-13318	US-09-897-214-8	US-09-737-149-29	US-10-135-322-19	US-09-815-242-11829	US-10-077-130-5	US-09-815-242-10744	US-10-078-770-158	US-09-866-582-38	US-09-815-242-12489	US-10-098-807-2	US-09-815-242-5407	US-09-918-508-2	US-09-966-614-2	US-09-853-918-37	US-10-267-311-21	US-09-918-951-4	US-09-738-626-5869	US-10-003-405-2	US-09-789-561-156	US-09-738-626-5963	US-10-092-880-9	US-09-770-107-2	US-09-815-242-13436	US-09-946-239-11
Sequence 12713, A Sequence 13318, A		Sequence 29, Appl	Sequence 19, Appl	Sequence 11829, A	Sequence 5, Appli	Sequence 10744, A	Sequence 158, App	Sequence 38, Appl	Sequence 12489, A	Sequence 2, Appli	Sequence 5407, Ap	Sequence 2, Appli	Sequence 2, Appli	Sequence 37, Appl	Sequence 21, Appl	Sequence 4, Appli	Sequence 5869, Ap	Sequence 2, Appli	Sequence 156, App	Sequence 5963, Ap	Sequence 9, Appli	Sequence 2, Appli	Sequence 13436, A	Sequence 11, Appl

ALIGNMENTS

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L 300	241 FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL	Qy 2	
240	181 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG	Db 1	
••	181 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240	Oy 1	
	121 QGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT 180	Db 1:	
180	121 QGLDITTILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT	Qy 1:	
•	61 TSPQLSRESMYKLSINHLTIQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLL 120	. Db	
·	61 TSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLL 120	Qy	
	1 MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAMKWTDVKL 60	Db	
_ [,	1 MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNAREYAIVKPINEEVKPESWAWKWTDVKL 60	Qy	
Ď.	vative 0;	Match	
	Query Match 100.0%; Score 2581; DB 10; Length 505;	Query	

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APPLICANT: Falco, S. Carl

APPLICANT: Famodu, Omolayo O.

TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
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                                                                                                                                                                                                                                                            US-09-909-745-24
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 24, Application US/09909745
Patent No. US20020119546A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application UP Patent No. US20020119546A1
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                                                     CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
                                                                                                                             APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
NUMBER OF
                 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                 APPLICANT: Falco, S. Carl APPLICANT: Famodu, Omola
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nes 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      DSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVLALLVREDPHGVCLE 486
                                                                                                                                                                                                                                                                                                                                                                                                                         SCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEPESQTQLL 427
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; ORGANISM: Oryza sativa 
US-09-909-745-20
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                                                                                                                NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office
SEQ ID NO 20
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09909745 Patent No. US20020119546A1
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Matches 155;
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                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                APPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: Squalene SFILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Falco, S. APPLICANT: Famodu,
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TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 NSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 MLRIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGYLLAGVPGAGGFDAIFAITLGDSG 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 QAQGKIGSGFDVAAAAYGSIRYRRFPPALIS------NLP---DIGSATYGSKLAHLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 LAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 KPNMDDYCNRNLFVIDIFSDD--AYHSQEDS-----VTEHRG------NRRLSFHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINE-----EVKPESWAWK---W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKLTQAWSSH--NVLALLVREDPHGVCLESGDPRT 492
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8.4%;
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Score
Pred.
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216; DB 10;
No. 8.5e-12;
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                  Length 67;
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Best Local Similarity

Matches

39;

Conservative

12;

Mismatches

14;

Indels

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; TYPE: PRT
; ORGANISM: Zea mays
US-09-909-745-18
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US-09-909-745-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity 74.18;
                                                                                                                                                                                                                     SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application (Patent No. US20020119546A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Patent No. US20020119546A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-909-745-18
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                                                                                                                                                                                                                                                        PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                         SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 REAMLRIRILMROMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAI
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                 397 REAMLRIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAI 450
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                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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RDACLEIRLHMREMGIAAGVPIEPDSQTRLLDATMNMEGVLLAGVPGAGGFDAV 54
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74.18;
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                                                                    Score 204; DB 10;
Pred. No. 6.8e-11;
8; Mismatches 6;
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Pred. No. 6.8e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Prokaryotes
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                                    360
                                                                      216 LLIGWTGS-PASTSDLVDRV---HQSKEEKQAAYEQFLMKSRLCVETMINGFN-----
                                                                                                          300
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                                                                                                                                                                               241 FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT-EFSLPPLMN 299
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                                                                                                                                                                                                                                                                                                                                123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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APPLICATION NUMBER: 60/
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                                  DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE 419
                                                                                                          LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                           GDIAASCYGG--WIAFSTFDHDWVNQKVT----TETLTDLLAMDWPELMIFPLKVPKQLR 215
                                                                                                                                                                                                                     GSSGAVTVGTVKALNIFYDLGL:
                                                                                                                                                                                                                                                      GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240
                                                                                                                                                                                                                                                                                                                                                                     ---RRNGELVLDIR--
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                                                                                                                                                                                                                                                                                            ----SFYHLK-----RKYGL 117
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Yamamoto, Robert T.
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TGKIS-VIQKQITKNRQ-----LLAELSSLTGVVIE
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Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                     -ENPF----HYVLAAIHL-TEKYAQEQNKEL---
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
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218 EVLIGWTGSPASS-PHFVSEVKRLK-SDP
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                                                                                                                                                                                                                                                                                                                       63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
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APPLICATION NUMBER: 60/191,078
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                                                                                                                                            GLGSSAAVLVSVIKVLNEFYDM-------KLSNL-YIYKLAVIANMKLQSLSSCG
                                                                                                                                                                             GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
                                                                                                                                                                                                                  LNYVVTAIEIFEQYAKSCDIAMKHFHLTIDS-----NLDDSNG------HKY 118
                                 NLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDH
                                                                                                      FDVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLM
                                                                                                                                                                                                                                                                                                                                                           IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRF--VTATIEE-----TD----
                                                                     -DIAVSVYSGWLAYSTFDHEWVKH-QIEDT--
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o. US20020061569A1
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                                                                   ----TVEEVLIKNWPGLHIEPLQAPENM
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LENGTH: 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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166
                                245 CAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMNLFL 302
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                                                                                                            185 SAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVS
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                                                                                                                                                                                                                                40 ---QYKGTIHSKALHHNPVTFSRD---EDSI--VISDPHAAKQ-----LNYV 78
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                                                                        SAAVLVSVIKVLNEFYDM-
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Xu, H. Howard
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                                                                        -----KLSNL-YIYKLAVIANMKLQSLSSCG-DIA
                                                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 133.5; DB Pred. No. 0.0016;
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-TVEEVLIKNWPGLHIEPLQAPENMEVLI
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TITLE OF INVENTION: Squalene Synthesis En:
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
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VSHATIETVLRTTL--
                                                                                                                                                                                                                           VGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVT----GLPLNEVIGTILKGKWDNKRTEF 292
                                                                                                                                                                                                                                                                                                             -TGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEG--KFGCSDLDVIHMIAQTSHCLAQGK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESMYKLSLNHLTLQ-SVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDI 125
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                             AASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAI 453
                                                                                                  KLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGE 412
                                                                                                                                    ------IMAFVFSAVDSISNELT
                                                                                                                                                                   SLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLS
                                                                                                                                                                                                         -PSGIDNTVSAYGN---
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Pred. No. 0.3084;
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                                                                                                                                                                          Sequence 8, Application US/09925388 Publication No. US20030054523A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Office 97 SEQ ID NO 23
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Best Local Similarity
APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: ISOPRENOID PRODUCTION
FILE REFERENCE: ISOPRENOID PRODUCTION
CURRENT APPLICATION UMBBER: US/09/925,388
CURRENT FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR APPLICATION NUMBER: 60/107,241
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APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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                                                                                                                                                                                                                                                                                                                                                          RIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGT 460
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Pred. No. 0.015;
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                                             US-10-092-880-4
                                                                                                      SEQ ID NO 4
LENGTH: 1477
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Query Match
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                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/092,880 CURRENT FILING DATE: 2002-03-08 PRIOR APPLICATION NUMBER: 09/155,614 PRIOR FILING DATE: 1998-09-30 PRIOR APPLICATION NUMBER: 08/617,697 PRIOR FILING DATE: 1996-04-01
                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US97/04707
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
                                                               ORGANISM: Haemophilus influenzae
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Score 108.5;
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Length 1477;
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                                                                                                                                                                                NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 534
TYPE: PRT
                                                                      Matches
                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZHOU, XIA-DI
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: IMMUNMODULATION
FILE REFERENCE: 3053-4071US3
                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 202-02-15
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MIKESELL, APPLICANT: CHANG, H
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                                183 GSSAAMTTAVVAALLHY-----LGVVDLSDPCKEGKFGC------SDLDVIHMI 225
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GSAYANRTALFPDLLAQGNASLRLQRVRVAD---EGSFTCFVSIRDFGSAAVSLQVAAPY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNAAESNGA-NSKPEVAKTG----LGSSAAMTTAVVAALL-----HYLGVVDLSDPCKE
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B; Mismatches
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	324 252	SMVGAVKKWQM : SPTGAVEVQVP	QDAHSSVTITPQR	GKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQM : :: : :	83 GKWDNKRTEFSLPPLMNLFLGEPG- : : : : 3 SQMANEQGLFDVHSILRVVLGANGT	Qy 2 Db 1
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23;	ps	534; · 145; Ga	DB 10; Len ; 136; Inde	3.9%; Score 101.5; 22.8%; Pred. No. 1.9 ive 48; Mismatches	Match Local Similarity (es 97; Conservat	Query M Best Lo Matches
					ORGANISM: Homo sapiens 9-875-338-7	; ORGAN US-09-875
					7 534	; SEQ I
				2.1	NUMBER OF SEQ ID NOS: 94 SOFTWARE: Patentin Ver. 2.1	NUMBER
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				06-06 0/272,107	FILING DATE:	; CURRENT ; PRIOR AF
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	FOR	rides userul	S AND POLYPEPTIDES	B7-RELATED NUCLEIC ACIDS IMMUNOMODULATION	OF INVENTION: B	; TITLE
				ð		APPL
		·			APPLICANT: YANG, GUCHEN	, APPL
•				13	: CHANG, H	, APPL
	•			1	NO. US20020095024	; Patent ; GENERAL
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	446	VPGAGG	-MSAEGVLLAG	DST		. 4
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	414	AA	ILMROMGEAA-	AIIKELLEAREAMLRIR	184 PINEAIIKE	ду з
	299	LTDTKQLVHSFTE	LNLIWQLTI	-TDATLRCSFSPEPGFSLAQ	253 EDPVVALVGTDAT	Db 2
	383	SEKWVLHA-TE	VYLRVIKSCSVLTS	SDPEKARENWONLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHA-TE	325 SDPEKARENWONLSDAN	0у з
	252	-SMYGAVKKWQM : RSPTGAVEVQVP	SGGSSTPS : CDAHSSVTITPQRS	SOMANEOGLEDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVTTTPQRSPTGAVEVQVP	193 SQMANEQGLEDVHSILRVVLGANGT	Db 1
	192	PLTGNVTT	PEAEVFWQDG-QGVPLT-	YQGY		
	282		EVLSFAQVAVTGLE	SORYVRFS	AQTSHCLAQGK-	

Search completed: April 26, 2003, 13:02:22 Job time: 22 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

654321	Result No.
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100.0 74.8 74.8 61.2 61.2 59.3	Query
505 507 511 496	Query Match Length DB ID
23 1 24 26 27 27	1 DB
US-09-988-863A-2 PCT-US02-24048A-12 US-10-036-959B-12 US-10-219-999-40847 US-0-324-109-16899 US-09-708-427-83408	ID
Sequence 2, Appli Sequence 12, Appl Sequence 12, Appl Sequence 40847, A Sequence 16899, A Sequence 83408, A	Description

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Sequence 22, Appl sequence 23, Appl sequence 3406, Ap sequence 3406, Ap sequence 3406, Ap sequence 8406, Ap sequence 177, App sequence 177, App sequence 178, App sequence 104, App sequence 104, App sequence 7023, Ap sequence 7023, Ap sequence 13279, A sequence 13279, A sequence 17922, A sequence 17922, A sequence 17922, A sequence 24, Appl sequence 1100, Ap sequence 24, Appl sequence 1100, Ap sequence 24, Appl sequence 1100, Ap sequence 1100, Ap sequence 1100, Ap sequence 1100, Ap sequence 11100, Ap sequence 11100, Ap sequence 11100, Ap sequence 28517, Apsequence 28517, Apsequence 28517, Ap sequence 28517, Appl sequence 38517, Appl sequence 38	equence 8340 equence 6622 equence 6622 equence 6622 equence 6520 equence 5500 equence 6220 equence 6222 equence 5281 equence 5282 equence 5282

ALIGNMENTS

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61 TSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLL 120 	1 MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL 60 	US-09-988-863A-2 US-09-988-863A-2 US-09-988-863A-2 Sequence 2, Application US/09988863A GENERAL INFORMATION: APPLICANT: Bayer AG TITLE OF INVENTION: Plant phosphomevalonate kinases FILE REFERENCE: Le A 35 018 CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2 LENGTH: 505 TYPE: PRT ORGANISM: Arabidopsis thaliana US-09-988-863A-2 Query Match Best Local Similarity 100.0%; Score 2581; DB 23; Length 505; Best Local Similarity 100.0%; Pred. No. 1.1e-246; Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps

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Matches 374
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GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours & Company
TITLE OF INVENTION: Genes Involved in the Bic
TITLE OF INVENTION: brasiliensis Latex
FILE REFERENCE: CL1792 PCT
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/307,637
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 12
SEQ ID NO 12
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            GFDVSSAVYGSHRYVRFSPEVLSSAQDAGKGIPLQEVISNILKGKWDHERTMFSLPPLMS
                                                            TGLGSSAAMTTAVVAALLHHLGLVDLSSSCKEKKF--SDLDLVHIIAQTAHCIAQGKVGS
                                                                                                             LQGLDITILGTNDFYSYRNEIEACGLPLTPESLAALPSFSSITFNVEEANGQNCKPEVAK
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SOFTWARE: Microsoft Office 9
SEQ ID NO 12
LENGTH: 503
TYPE: PRT
ORGANISM: Heyea brasiliensi.
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Best Local Similarity 74.1
Matches 374; Conservative
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PRIOR EILING DATE: 2001-07-25
NUMBER OF CONT.
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CURRENT APPLICATION NUMBER: US/10/036,959B
CURRENT FILING DATE: 2002-05-10
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US-10-219-999-40847
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SEQ ID NO 40847
LENGTH: 511
TYPE: PRT
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Local Similarity 62.6%;
les 321; Conservative 6
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Stein, Joshua
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RESULT 6
US-09-708-427-83408
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SEQ ID NO 16899
LENGTH: 511
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TITLE OF INVENTION: CONA SEQUENCES AND USI
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
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ORGANISM: Zea mays
FEATURE:
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                                                           LPLLVREDCRGVSLEDADPRTREVSAAVSSIQI
                                                                                                                                               EAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNV
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Kovalic, David K.
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Sequence 83408, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CUGRENT APPLICATION NUMBER: US/09/708,427
CUGRENT FILING DATE: 2000-11-09

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APPLICANT: N. ALEXANDROV et al
                                                                        SEQ ID NO 83407
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                                                                                        FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
               ORGANISM: Zea
                                          TYPE: PRT
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     FEATURE:
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313; Conserv
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PatentIn version 3.1
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Pred. No. 3.2e-142;
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NAME/KEY: misc_feature
: LOCATION: 1.535
: OTHER INFORMATION: Ceres
US-09-708-427-66289
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NAME/KEY: misc_feature LOCATION: 1..535
OTHER INFORMATION: Xaa

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TYPE: PRT
ORGANISM: Zea mays subsp.

LENGTH: 535

FEATURE:

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NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version SEQ ID NO 66289
                                                                                                                                          Sequence 66289, Application US/GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al
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Best Local :
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OTHER INFORMATION: Xaa i NAME/KEY: misc_feature LOCATION: 1.535
                                                   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243 PCURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09
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; Pred. No. 3.7e-142;
68; Mismatches 108;
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Best Local S
Matches 277
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                                                                                                                                                                                                                                                                                           SEQ ID NO 66290
LENGTH: 326
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NAME/KEY: misc_feature
LOCATION: 1..326
OTHER INFORMATION: Xaa is
NAME/KEY: misc_feature
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OTHER INFORMATION: Ceres S
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
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                                                                   GANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCS--DLDVIHMIAQ 227
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                                        GEKCKPEVAKTGLGSSAAMTTSVVAALLHYLGVVSLSCPGQSSGDNTTRRELDLVHSIAQ 62
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Pred. No. 2.9e-123;
il; Mismatches 103;
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Best Local Similarity
Matches 198; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 83409
LENGTH: 326
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OTHER INFORMATION: Xaa i NAME/KEY: misc_feature LOCATION: 1.326
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TYPE: PRT
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                                                                                                                      LRILKGLSENHREAY - - -
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US-09-708-427-66291
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al
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SEQ ID NO 66291
LENGTH: 306
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Best Local Similarity
                                                                        APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                             APPLICANT: Cao, APPLICANT: Edge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
            PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
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 NUMBER OF SEQ ID NOS: 63520
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                                                                                                                                                                 Hinkle, Gregory J
Kovalic, David K.
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                                                                                                                                                   Liu, Jingdong
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Pred. No. 5.2e-80;
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Matches
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LENGTH: 286
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LENGTH: 281
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; TYPE: PRT; ORGANISM: Zea mays; US-10-219-999-55015
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US-10-219-999-42346
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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TITLE OF INVENTION: CDNA SEQUENCES AND USES
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
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PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
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405 ILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQ 464
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                                                                                     ETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIR 404
                                                                                                                                      WDHENKQFSLPPLMTLLLGEPGTGGSSTPSMYGSYKRWLKSDPEKSRDTWSKLAIANSTL 120
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                                              ENQLRILKGLSENHHEAYESMVRSCSRLTYGKWAEVATNQHQELIIRSLLAARDACLEIR
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US-09-708-427-65887
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US-60-312-544-6223
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                                                                                                                                             Sequence 65887, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65887
LENGTH: 359
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NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 6223
LENGTH: 281
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CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
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                       TYPE: PRT
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ORGANISM: Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLEL
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                                                                                                                                                                                                                                                                                                                                                                            AWSSHNVLALLVREDPHGVCLESGDPRTTCITSGVSSIHL 504
                                                                                                                                                                                                                                                                                                                                                                                                                 LHMREMGIAAGVPIEPDSQTRLLDATMNMEGVLLAGVPGAGGFDAVFSVVLGDASNAVAH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENQLRILKGLSENHHEAYESMVRSCSRLTYGKWAEVATNQHQELIIRSLLAARDACLEIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinkle, Gregory J.
Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/60312544
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59.3%;
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 27;
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; NAME/KEY: misc_feature
; COCATION: 1..359
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..359
; OTHER INFORMATION: Ceres Seq. ID 1929648
US-09-708-427-65887
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Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                109 EKDKES---LHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNA 165
                                                                                                                                                                                                                                        114 DSWTWAWTDVKXTSPQLSRVATYKLSLNKTTLQLTSSRESTNPFVEQAIQFSVAAAK-AT
293 DLVHTIAQSAHCLAQGKIGSGFDVSAAVYGSQRYVRFSPEILSSAQ-AIGG 342
                                                                                                                                                             173 IIDKERKDVVDKLLLQGLNITIIGHNDFYSYRKQIEARGLPLTPEVLLSLPPFSSITFNS
                                                                                                                                                                                                                                                              49 ESWAWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLAT 108
                    DVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTG
                                                                                EVANGTMTGEKCKPEVAKTGLGSSAAMTTSVVAALLHYLGAVNLSCPGQSSGDNASGREL
                                                                                                   AESNGA----NSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCS--DL
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                    28.0%; Score 722.5; DB 66.2%; Pred. No. 5e-62; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                Length
                                         279
                                                                                                                                                                                                                                                                                                                                                                359;
                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                      Gaps
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Search completed: April 26, 2003, 13:00:27
Job time: 151 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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               Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/paa/F
2: /cgn2_6/ptodata/2/paa/F
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4: /cgn2_6/ptodata/2/paa/F
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/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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US-10-369-493-1209
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Sequence 3218, Ap
Sequence 22, Appl
Sequence 3740, Ap
Sequence 2162, Ap
Sequence 13279, A
Sequence 24, Appl
Sequence 1909, Ap
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	Appli	6734, Ap	57799, A	69748, A	67, Appl	106, App	28143, A	21583, A	3, Appli	17298, A	11755, A	14927, A	73, A	14445, A	18348, A	20380, A	1315, Ap	10690, A	43911, A

ALIGNMENTS

RESULT 1 PCT-US02-40225-3218

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SEQ ID NO 3218
LENGTH: 501
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CURRENT FILING DATE: 2002-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Eroshkin, Alexey M.
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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                                                                                                             KPESWAWKWTDVKLTSPQLSRES---MYKLSLNHLTLQSVSASD-----
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LENGTH: 179
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                            APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Grea
APPLICANT: Slater, Ste
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
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SOFTWARE: Microsoft Office
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PRIOR FILING DATE: 1998-11-05
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                              Gregory J. Steven C.
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Pred. No. 2.5e-44;
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US-10-369-493-3740
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Sloter, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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SEQ ID NO 3740
                                                                                                                                                                                                                          Sequence 2162,
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Best Local Similarity
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLP-----L 273
                                                                                                                                                                                                                                                                                                                                                FAITLGDSGTKLTQAWSSHNVLALLVRED 479
                                                                                                                                                                                                                                                                                                                                                                                                    ELLEAREAMLRIKILMRQMGEAASVPIEPESQTQLLDS-TMSAEGVLLAGVPGAGGFDAI 450
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                                                                                                                                                                                                                                                                                                                                                                               ---EIRPAVHAIRELVRKMGTESGVPIEPDSQKELLDALEEGVEGVYGGVVPGAGGYDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENWONLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEVIGTILKGKWDNK--RTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172;
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: ||||||| ||: ||: || ||| : ||: ||: ||
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Pred. No.
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                   ORGANISM: Aspergillus fumigatus US-09-675-784A-13279
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SEQ ID NO 2162
                                                                                    NUMBER OF SEQ ID NOS: 13925
SEQ ID NO 13279
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                                                                                                                                                                                      TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC TITLE OF INVENTION: AND USES THEREFOR FILE REFERENCE: 2976-4020US1
                                                                                                                  PRIOR FILING DATE: 1999-09-29
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/675,784A CURRENT FILING DATE: 2000-09-29
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                                                                  LENGTH: 491
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GREENE, JONATHAN R.
                                                                                                                                                                                                                                                                         KESSLER, MARCO
NOLLING, JORK
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; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2162
                                                                                              Sequence 13279, Application US/09675784A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 VPFQLPATYCLLMGDV-AGGSSTPGMVKKVQQWQKENPEESK----NCFD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 CWQDLQVTLQVDNAYY-HQPQ-----LKPDQ--TSYPKFNFLNCTLG-------
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                                                                                                                                                                                                                                                                                                                                                             WSSHNVLALLVREDPHGVCLE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV----AVTGLPLNEVIGTILKGKWDNKR 289
                                                                                                                                                                                                                                                                                                WKDDGVVPMDVSPAFDGLAVE 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG--TKLTQA 465
                                                                                                                                                                                                                                                                                                                                                                                                                          ---EAKVDIEPLKQTNILDNIEQLPGVIGVGVPGAGGFDAQFCLAINHTEIIENVIKT 402
SHAW, KAREN J.
SHIMER JR., GEORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DLYSRVLSIKNCFL-
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Pred. No. 1.8e-35;
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APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/433,242
PRIOR APPLICATION NUMBER: 09/433,242
PRIOR APPLICATION NUMBER: 09/437,241
PRIOR FILING DATE: 1999-11-04
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
COPTUALES: MICHOSEP: MICHOSEPE OF COPTUALES: MICHOSEPE OF 
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US-09-909-745A-24
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                                                                                                                                                                                                              US-09-909-745A-24
                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft
SEQ ID NO 24
LENGTH: 451
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                                                                                         72;
                                                                                   Score 453.5; DB 5;
Pred. No. 1.5e-32;
2; Mismatches 185;
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                                                                                           MLRIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG 459
                                                                                                                                                                                                                                                        HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDVKLTSPQLSRESMYKLSLNHLTLQS----VSASDSRNPFVEHAIQYAIAAAHLATEKD
                            TKLTQAWSSH--NVLALLVREDPHGVCLESGDPRT 492
                                                            VATIRRSFRKITKESGADIEPPVQTSLLDDCQTLKGVLTCLIPGAGGYDAIAVITKQDVD
                                                                                                                         SRFMDGLSKLDRLHETHDDYSDQIFESLERNDCTCQKY----
                                                                                                                                               LELETKLNDLSKLAKDHWDVYLRVIKSC--SVLTSEKWVLHATEPINEAIIKELLEAREA
                                                                                                                                                                                         EEDWNITIKSNHLPSGLTLWMGDI-KNGSETVKLVQKVKNWYDSHMPESLKIYTELDHAN
                                                                                                                                                                                                                    ---WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN 341
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В Q Вb Q DЬ Q ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-1909 PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1909
LENGTH: 451 Sequence 1909, GENERAL INFORMATION: Query Match -10-369-493-1909 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28 APPLICANT:
APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao, TYPE: PRT 112 KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171 102 KPNMDDYCNRNLFVIDIFSDD--AYHSQEDS---/ Match 17.6%; Local Similarity 30.1%; nes 155; Conservative 7. 56 æ 6 SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINE-----EVKPESWAWK---W TDVKLTSPQLSRESMYKLSLNHLTLQS----VSASDSRNPFVEHAIQYAIAAAHLATEKD 111 Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng Application Yongwei -LYHISPKSGFIPVSIGGSKNPFIEKVIANVFSYF-----US/10369493 Score 453.5; DB 6 Pred. No. 1.5e-32; '2; Mismatches 185 -VTEHRG-DB 6; 185; Length Indels 103; IN PLANTS FOR 451; NKRLSFHS 144 Gaps PRODUCTION 101 55 18;

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US-09-909-745A-16
; Sequence 16, Application US/09909745A; GENERAL INFORMATION:
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US-09-909-745A-20
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                                                                                                                                                                                                                    RESULT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                       APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
              CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/433,242
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
                                                                                                                    APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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PRIOR FILING DATE: 1999-11-04
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Pred. No. 2.8e-12
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Best Local Similarity
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US-10-282-122A-56929
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US-09-909-745A-18
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SEQ ID NO 18
LENCTH: 54
TYPE: PRT
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SEQ ID NO 16
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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TITLE OF INVENTION: Squalene:
FILE REFERENCE: BB1112 US CIP
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                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in
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les 40; Conserv
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                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                  Yamamoto, R. Forsyth, R.
                                                                                                                                                                 Carr, Grant
                                                                                                                                                                                    Trawick, John
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Haselbeck, Robert
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74.1%;
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Pred. No. 2
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US-10-282-122A-56929
Sequence 5356, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO:
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 0329
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 368
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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ETILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/
FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-0: APPLICATION NUMBER: FILING DATE: 2000-0:
                                                                                                                                                                                                                                                    TEALKNLCDLAESYTGA--AKSSGAGGGDCGIVIFRQKSGILPLMTAWEKDGITPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .GDIAASCYGG--WIAFS----TFDHDWVNQKVATETLTDLLAMDWPELMIFPLKVPKQLR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240
                                                                                                                                                                                                                                                                                                                                                                              DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE 419
                                                                                                                                                                                                                                                                                                                                                                                                                       LLIGWTGS-PASTSDLVDRV---HQSKEEKQAAYEQFLMKSRLCVETMINGFN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
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22.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 177.5; DB 6;
Pred. No. 1.6e-07;
58; Mismatches 179;
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RESULT 14 US-09-134-000C-5356

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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5356
LENGTH: 370
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297
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 TEALKNLCDLAESYTGA--AKSSGAGGGDCGIVIFRQKSGILPLMTAWEK:GITPL
                                 PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL
                                                                                                     DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE
                                                                                                                                        LLIGWTGS-PASTSDLVDRV---HQSKEEKQAAYEQFLMKSRLCVETMINGFN-----
                                                                                                                                                                                                                                                                                                                 GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240
                                                                                                                                                                                                                                                                                                                                                                                      LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                               PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
                                                                                                                                                                       LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW 359
                                                                                                                                                                                                          GDIAASCYGG--WIAFS----TFDHDWVNQKVATETLTDLLAMDWPELMIFPLKVPKQLR
                                                                                                                                                                                                                                                                                GSSGAVTVGTVKALNIFYDLGL - -
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                                                                    TGKIS-VIQKQITKNRQ-----LLAELSSLTGVVIE
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Pred. No. 1.7e-07;
8; Mismatches 179;
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 350
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                                                                                                       419
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
                                                                                                                                                                                                           SEQ ID NO 5356
LENGTH: 370
                                                                                 Query Match
Best Local Similarity
                                                               Matches
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
                                                                                                                                                                                     TYPE: PRT
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VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 : | | | : | | : | : | : | : |
                                                               106;
                                                               Conservative
                                                                              6.9%;
                                                               58;
                                                                              Score 177.5; DB 5; Pred. No. 1.7e-07;
                                                             Mismatches 179;
                                                               Indels 133;
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                                                               Gaps
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	351	QY 292 FSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDL
	291 208	Qy 233 AQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE- :
	155	YQGKKIGLGSSGAVTIAVIRGLSLLYDLHLKDIDIFKLAAIAHIQ
	232	PCKEGKFGCSDLDVIHMIAQTSHCL
	110	82KSYGIQIKSQLD
	177	119 LLOGIDITTIGSNDEVSYRNOTESAGIDITDESIGTIADEASITENAAESNGANSKDEV-
	118 81	OY 59 KLTSPOLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKL Db 66
	65	: : : : : :
,02	reaps	O/; MISHMCCHES 108; INGELS 108;
3		atch 6.0%; Score 154; DB 1; Length 362; cal Similarity 20.8%; Pred. No. 2.2e-05;
		ORGANISM: Alloiococcus otitidis PCT-USO2-36122-42
		362 362
		OF SEQ 1
		ENT APPLICATION N
	0,	; APPLICANT: Murphy, Ellen and Projan, Stephen, j.; TITLE OF INVENTION: Allolococcus otitidis Infectious Disease Targets
		PCT-USO2-36122-42 ; Sequence 42, Application PC/TUSO236122 ; GENERAL INFORMATION:
		15
		Db 297 TEALKNICDLAESYTGAAKSSGAGGDCGIVIFRQKSGILPLMTAWEKDGITPL 350
		QY 420 PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL 474
4.	296	267LLAELSSLTGVVIE
	419	QY 360 DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE
	266	Db 218 LLIGWTGS-PASTSDLVDRVHOSKEEKQAAYEQFLMKSRLCVETMINGFN
) t	200 1 01 000000000000000000000000000000
	299	QY 241 EVYSCAVIGSQKIVKESEBVIJSERQVAVIGLENJEVIGTLIKGRWUNKET EESLEPLIM
	163	120 GSSGAVIVGIVAALNIRTULGIENEELFKLSALAHLAVQGN-GSC
	240	183 GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
	119	Db 99SFYHLKRKYGL
	182	Qy 123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL
	98	63RRNGELVLDIRENPFHYVLAAIHL-TEKVAQEQNKEL
	122	
	62	Db 4 IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-

Search completed: April 26, 2003, 13:01:55 Job time: 84 secs

THE PACE BLANK (118PTO)